



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 110600

To: Sarvamangala Devi
Location: CM1/7E15
Art Unit: 1645
Thursday, December 18, 2003

Case Serial Number: 09/428122

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

Shears, Beverly

110600

From: Devi, Sarvamangala
Sent: Tuesday, December 16, 2003 10:17 AM
To: Shears, Beverly
Subject: 09/428,122

Beverly:

Would you please perform a sequence and an interference search for SEQ ID NO: 1 and SEQ ID NO: 2 in application 09/428,122? Please also run SEQ ID NO: 1 against the amino acid sequence.

Thanks.

S. DEVI, Ph.D.
AU 1645
CM1-7E15



SEARCH REQUEST FORM

Requestor's

Name: _____

Serial

Number: _____

Date: _____

Phone: _____

Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 12-17-03

Search Site

Version

SEARCH REQUEST FORM

Requestor's

Name:

Devi

74495

Serial

Number:

09/428,122

Date:

12/3

Phone:

308-9347

Art Unit:

1040

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

A 519 A Seq 1 vs A 81535

(1)

Seq 1

MUST BE

SCANNED.

75.8
100

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 12:14:27 ; Search time 10698 Seconds
(without alignments)
11472.133 Million cell updates/sec

Title: US-09-428-122-1
Perfect score: 3000
Sequence: 1 cgccttacctagtagaggt.....tggtttgtaaacactttc 3000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_em.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_or.*

21: em_ov.*

22: em_pat.*

23: em_ph.*

24: em_pi.*

25: em_ro.*

26: em_sts.*

27: em_un.*

28: em_vi.*

29: em_hum.*

30: em_hum.*

31: em_hum.*

32: em_hum.*

33: em_hum.*

34: em_hum.*

35: em_hum.*

36: em_hum.*

37: em_hum.*

38: em_hum.*

39: em_hum.*

40: em_hum.*

41: em_hum.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 2988 | 99.6 | 16448 | 1 | AE001587 | AS001587 Chlamydia |
| 2 | 2988 | 99.6 | 26920 | 1 | CPN133035 | AJ133035 Chlamydia |
| 3 | 2986.4 | 99.5 | 12127 | 1 | AE002235 | AE002235 Chlamydia |
| 4 | 2986.4 | 99.5 | 299650 | 1 | AP002545 | AP002545 Chlamydia |
| 5 | 2975.4 | 99.2 | 110000 | 6 | AR310754_00 | AR310754 Sequence |
| 6 | 2775.8 | 92.5 | 2787 | 6 | AR1835 | AR1835 Sequence 9 |
| 7 | 2241 | 74.7 | 2241 | 6 | AX349497 | AX349497 Sequence |
| 8 | 570.4 | 19.0 | 300512 | 1 | AE016995 | AE016995 Chlamydia |
| 9 | 546.6 | 18.2 | 2781 | 6 | AX662119 | AX662119 Sequence |
| 10 | 546.6 | 18.2 | 2781 | 6 | AX666191 | AX666191 Sequence |
| 11 | 546.6 | 18.2 | 4926 | 1 | CPU72499 | U72499 Chlamydia |
| 12 | 531.8 | 17.7 | 12676 | 1 | AE002192 | AE002192 Chlamydia |
| 13 | 531.8 | 17.7 | 300650 | 1 | AP002546 | AP002546 Chlamydia |
| 14 | 531.2 | 17.7 | 10757 | 1 | AE001628 | AE001628 Chlamydia |
| 15 | 530.2 | 17.7 | 2815 | 6 | AR1829 | AR1829 Sequence 3 |
| 16 | 530.2 | 17.7 | 17280 | 1 | CPN133034 | AJ133034 Chlamydia |
| 17 | 527 | 17.6 | 2787 | 6 | AX349573 | AX349573 Sequence |
| 18 | 523 | 17.4 | 534 | 6 | AX349495 | AX349495 Sequence |
| 19 | 522.2 | 17.4 | 2757 | 6 | AR1837 | AR1837 Sequence 11 |
| 20 | 518.4 | 17.3 | 10026 | 1 | AE002193 | AE002193 Chlamydia |
| 21 | 518.4 | 17.3 | 110000 | 6 | AR310754_05 | Continuation (6 of |
| 22 | 518.4 | 17.3 | 300650 | 1 | AP002546 | AP002546 Chlamydia |
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| 25 | 516.6 | 17.2 | 17280 | 1 | CPN133034 | AJ133034 Chlamydia |
| 26 | 515.2 | 17.2 | 15068 | 1 | AE001627 | AE001627 Chlamydia |
| 27 | 515 | 17.2 | 2787 | 6 | AR1839 | AR1839 Sequence 13 |
| 28 | 515 | 17.2 | 12676 | 1 | AE002192 | AE002192 Chlamydia |
| 29 | 514 | 17.1 | 2793 | 6 | AR1841 | AR1841 Sequence 15 |
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| 35 | 496.2 | 16.5 | 110000 | 6 | AR310754_04 | Continuation (5 of |
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| 38 | 465.8 | 15.5 | 6030 | 1 | CPOMP54 | AJ001311 Chlamydia |
| 39 | 378.4 | 12.6 | 2838 | 6 | AR1849 | AR1849 Sequence 23 |
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| 42 | 349.4 | 11.6 | 6234 | 1 | CPU65943 | U65943 Chlamydia |
| 43 | 348.8 | 11.6 | 10574 | 1 | AE001586 | AE001586 Chlamydia |
| 44 | 348.4 | 11.6 | 2520 | 6 | AX662085 | AX662085 Sequence |
| 45 | 348.4 | 11.6 | 2520 | 6 | AX666157 | AX666157 Sequence |

ALIGNMENTS

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DEFINITION Chlamydia pneumoniae section 3 of 103 of the complete genome.
ACCESSION AE001587 AE001363
VERSION AE001587.1 GI:4376271
KEYWORDS
SOURCE Chlamydia pneumoniae CWL029
ORGANISM Chlamydia pneumoniae CWL029
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia. Chlamydia.
REFERENCE 1 (bases 1 to 16448)
AUTHORS Kallman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R. W.,
Olinger, R., Grimwood, J., Davis, R. W. and Stephens, R. S.
TITLE Comparative genomes of Chlamydia pneumoniae and C. trachomatis
JOURNAL Nat. Genet. 21 (4), 385-389 (1999)


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MEDLINE 99206606
PUBMED 10192388
REFERENCE 2 (bases 1 to 16448)
AUTHORS Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Olinger,L.,
Grimwood,J., Davis,R.W. and Stephens,R.S.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1998) Program in Infectious Diseases, University
of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
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Db 1931 TAGGACTGCMACTTCAACTGGACTAAAACTGGCTATATTTCTTAATCCGAGGCTATCGG 1990
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| FEATURES | | source | |
|---|------|--|------|
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| AUTHORS | | | |
| JOURNAL | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| Submitted (21-JAN-1999) Boesen T., Department of Medical Microbiology and Immunology, University of Aarhus, The Bartholin Building, DK-8000 Aarhus, DENMARK | | | |
| Direct Submission | | | |
| Unpublished | | | |
| 2 (bases 1 to 26920) | | | |
| Boesen,T. | | | |
| Daugaard,L., Hjerno,K., Knudsen,K., Madsen,A.S., Christiansen,G. and Birkelund,S. | | | |
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Query Match 99.6%; Score 2988; DB 1; Length 26920;
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| Db | 19101 | TTTCAGAGGTACTCTATCTTTTAAACATGGAGTGACTCTGCAAGCTCAGGCAATTCACCTCA | 19160 |
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| Db | 19521 | TACGACTGCAACCTTCAACTGGACTAAACCTGGCTATATTCCTAATCCCGACGCTATCGG | 19580 |
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| Db | 20001 | CACCCATACGGATAAACGATCTGAAAAACCAAGTATACAAATATCTCTGTTTAAAGGAAG | 20060 |
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RESULT 3
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ACCESSION AE002235 AE002161
VERSION   AE002235.2 GI:8163495
SOURCE   Chlamydomophila pneumoniae AR39
ORGANISM Chlamydomophila pneumoniae AR39
REFERENCE 1 (bases 1 to 12127)
AUTHORS   Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Unayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
TITLE     Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
JOURNAL   Nucleic Acids Res. 28 (6), 1397-1406 (2000)
MEDLINE   20150255
PUBMED    10684935
REFERENCE 2 (bases 1 to 12127)
AUTHORS   Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Unayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
TITLE     Direct Submission
JOURNAL   Submitted (01-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
COMMENT   On Jun 1, 2000 this sequence version replaced gi:7189672.
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| Qy | 1801 | G | AAATTC | CAATACGGCTAT | CAGGAACTTGGGCCCAATGTTTGGGGACAGGGGCTTC | 1860 | |
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| DB | 22829 | TACGACTCGAACTTCCAATCGACTGAACTGAGTAACTGCTATATTCCTAAATCCCGAGCGTATCGG | 22888 |
| QY | 1921 | CCTTTAGTCCCTAATAGCTTATGGAAATGCATTTATAGATATTAGCTCTCTCCATTATCT | 1980 |
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VERSION A81835.1 GI:6731868
KEYWORDS unidentifed
SOURCE unidentifed
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2787)
AUTHORS Madsen,A. and Birkelund,S.
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Ratti, G. and Grandi, G.
AUTHORS
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REFERENCE 1 (bases 1 to 300512)

AUTHORS

Read, T.D., Myers, G.S., Brunham, R.C., Nelson, W.C., Paulsen, I.T., Heidelberg, J., Holzapple, E., Khouri, H., Federova, N.B., Carty, H.A., Umayam, L.A., Hatt, D.H., Peterson, J., Beanan, M.J., White, O., Salzberg, S.L., Hsia, R.C., McClarty, G., Rank, R.G., Bavoil, P.M. and Fraser, C.M.

TITLE

Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae

Nucleic Acids Res. 31 (8), 2134-2147 (2003)

JOURNAL

MEDLINE

PUBMED

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AUTHORS

Read, T., Myers, G., Brunham, R., Nelson, W., Paulsen, I., Heidelberg, J., Holzapple, E., Khouri, H., Federova, N., Carty, H., Umayam, L., Hatt, D., Peterson, J., Beanan, M., White, O., Salzberg, S., Hsia, R.-C., McClarty, G., Rank, R., Bavoil, P. and Fraser, C.

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Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae Res. 31 (8), 2134-2147 (2003)
Nucleic Acids Res. 31 (8), 2134-2147 (2003)
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Read, T., Myers, G., Brunham, R., Nelson, W., Paulsen, I., Heidelberg, J., Holzapple, E., Khouri, H., Federova, N., Carty, H., Umayam, L., Hatt, D., Peterson, J., Beanan, M., White, O., Salzberg, S., Hsia, R.-C., McClarty, G., Rank, R., Bavoil, P. and Fraser, C.
Direct Submission
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| Qy | 1388 | GAGCCGCAATTCATAAAATCTTACTTGAAGCTACTACAGCTGTAACTCTTTTCAGA | 1447 |
| Db | 23357 | CAAACTGCCGATGCCGACACTTAAAGACAGTATTACAGCGCTATCGCATTTAGCCT | 23298 |
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| Db | 23297 | GGAGAGCTTATCTTTAGAAACGGTGTGGAGTAGAGGCAAAAAGCTGTTTCGCAACACGG | 23238 |
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| Db | 23237 | GGCTCTCTAATTTTGATTGATGCAGGAACAAAGCTGCTCGGAAACAGAGATCTCAG | 23178 |
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| Db | 23177 | CTAACCAACCTGGCGATCAATCTTAATCTTTAGATGGAAACAAAATCGCTGTTATGCC | 23118 |
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| Db | 22997 | TCTGCAAAAGGAAGCATATACACGACAGATGTCTTAGCACAAACGACAGTTCTCTCTGCA | 22938 |
| Qy | 1805 | TTCCATTAGCGCTATC - AGGGAACTTTGGGCCCAAATTTGTTTGGGGGACAGGGGCTCTTAC | 1863 |
| Db | 22937 | CAACATTTATGGGTATCAAGGAAACTGGTCTCTCTTGGATTTACAGATAACGGCTCAGAT | 22878 |
| Qy | 1864 | G-----ACTGCAACCTTCAACTGACATAAACTGGCTATATTCCTTAATCCCGAG | 1912 |
| Db | 22877 | CCTAAAACAAACAGCTGTCTTTTACTGGAATAAAACGGGATACAATCTCAATCCTCTGAA | 22818 |
| Qy | 1913 | CGTATCGGCTCTTTAGTCCCTAATAGCTTATCGAATGCATTTATAGATATTTAGCTCTCTC | 1972 |
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| Qy | 1973 | CATTATCTTATGGA --- GACTGCAAAAGAAAGGTTTGCAGGGAGACCGTCTTTTGGTGT | 2029 |
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| Qy | 2030 | GCTGGATATCTAACTTCTTCATAGGATAGTACAATAACACAGACGGGGTTTGCCTAT | 2089 |
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| Db | 22577 | GTAGCTTCTGTTCAGCTATTTGGGAAAGACAAGGACTACCTTTGTAGCGAAAAATGCTGCA | 22518 |
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RESULT 10
AX666191

LOCUS AX666191 2781 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 56 from Patent WO0247718.
ACCESSION AX666191
VERSION AX666191.1 GI:29290994
KEYWORDS
SOURCE Chlamydomophila psittaci
ORGANISM Chlamydomophila psittaci
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
REFERENCE 1
AUTHORS Johnston, S.A.
TITLE Methods and compositions for vaccination comprising nucleic acid
ad/or polypeptide sequences of i(chlamydia)
JOURNAL Patent: WO 0247718-A 56 20-JUN-2002;
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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RESULT 11

CPU72499

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

4926 bp DNA linear BCT 13-MAY-1999
Chlamydomonada abortus putative outer membrane protein gene, partial
cds; and putative 98 kDa outer membrane protein gene, complete cds.
U72499
U72499.1 GI:1657776

Chlamydomonada abortus
Chlamydomonada abortus
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomonada.
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Longbottom, D., Russell, M., Dunbar, S.M., Jones, G.E. and Herring, A.J.
98kDa protein genes from ovine abortion strain S26/3 Chlamydia
psittaci
Unpublished

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REFERENCE 2 (bases 1 to 4926)
AUTHORS Longbottom, D.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-1996) Moredun Research Institute, 408 Gilmerton
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Dy 2324 TTTTGTTCAGACTGCAGACAACCTAACTTTCAAAGGGAAACAACCATAGCTTATCCATAAC 2383
Qy 388 AACGGTGGATCGAGGACTGTAGCAGGGCGTGTGTTAAACAGCAGCGGTGGTAGATAATC 447
2384 GAACGCGAATGCCGGAGCTAATCC---TGCGGGAATTAAAGTTAAACACTGCCGATAGAT 2440
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| QY | 1582 | TAA | CATCAG | TGTT | TATAG | ACGGT | CAAAAG | CGCAAAA | TAGAAA | CAACCAAG | CTAGCTCAAA | 1641 | | | | | | | | |
| DB | 3548 | TAATCCGA | ATACTT | AGATGG | AAAAAAT | TCGCGT | AGT | CGAT | CGCGT | TGCTGCT | CGGAA | 3607 | | | | | | | | |
| QY | 1642 | AAATCTG | ACTTTAT | CTG | GAACCA | CTACAT | TTAT | TGGA | CCGAC | GGCAG | CTTTTATG | AAAA | 1701 | | | | | | | |
| DB | 3608 | GAA | TGTGAC | TTTAT | CAG | TGCTA | TG | GGCGT | TATT | GATCCT | ACAGGA | TTTATG | AAAA | 3667 | | | | | | |
| QY | 1702 | TCATAG | TTTAA | GAATCCT | CAGT | CCTAC | GACAT | CTTAG | AGCT | CAAA | AGCTTCT | TGGA | CTGT | 1761 | | | | | | |
| DB | 3668 | CCATA | AGCTAA | TATG | ATCAG | TTAG | CTTTAG | GAG | GAAT | CAACTTTCT | CGG | AAAG | GTTC | CGGT | 3727 | | | | | |
| QY | 1762 | AAC | AGCAC | CCG | CAGT | GA | CTCCAG | ATCCT | TATA | ATGGGT | GAG | AAATTC | CAAT | TAC | GGCTATCA | 1821 | | | | |
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| QY | 1822 | GGG | AA | ----- | TTGGG | CCCA | ATG | TTTGG | GGG | CAC | AGG | GTCTT | CTAC | AG | TGC | 1869 | | | | |
| DB | 3788 | AGG | AACTGT | CTCTC | AGT | TTGGG | TCA | AGATA | TAATA | CTGT | GATCCT | TAAAC | ACAAAA | CAGC | | 3847 | | | | |
| QY | 1870 | AAC | CTTCA | CTGG | ACT | AAACT | GCTATAT | TCCT | TAATCC | GAGG | GTAT | CGG | CTCTTT | TAGT | | 1929 | | | | |
| DB | 3848 | AAT | CTTTAC | CTGG | AAATAA | ACAG | ATATG | TTCC | AAATCCT | GAAC | GTG | CTG | CTCG | CTAGT | | 3907 | | | | |
| QY | 1930 | CCCTAA | TAGCTT | TGGA | ATGCAT | TTT | TAG | ATAT | TAG | CTCTCT | CCCAT | TATCTT | TAT | TGG | AG | 1989 | | | | |
| DB | 3908 | ACT | CAATAG | CTTTGGG | ATCC | TTTATAG | ATTAG | TTTAC | GT | TTAT | TAAG | ATGTCT | TGGA | ACG | | 3967 | | | | |
| QY | 1990 | TG | CAAC | CGAA | GGT | TGC | ---AGG | GAG | ACCG | TGCTTTT | TG | TGTG | TGCT | GGAT | TATCA | ACTT | 2046 | | | |
| DB | 3968 | TAG | TGTTG | TAG | TATCT | TGAG | CAC | GTCTG | TGGT | TTCTG | TGGT | CTCTG | GAAT | TGG | AACTT | | 4027 | | | |
| QY | 2047 | CTTCC | ATAAG | TAGTACA | AAAA | CAC | AG | CGGG | TTTCG | CCATTT | TG | AGTGG | CGG | TTT | ANGT | | 2106 | | | |
| DB | 4028 | CTTCC | ATAAG | ATCG | GAATCG | TAAAA | TCG | AAATTC | CGT | CAT | ATCAG | TTCTG | GGAT | TATG | | | 4087 | | | |
| QY | 2107 | CAT | AGG | AGG | AAACCT | CTAT | CTTGT | CAG | ATAAG | ATTCTT | TAG | TGCTG | CTCAT | TTTGT | CTAG | CT | 2166 | | | |
| DB | 4088 | GTT | AGG | ACCA | CAACA | ATCCT | CG | AGAG | AGATCT | CTT | TAGT | TG | GGCTTCT | TGT | CAG | TT | 4147 | | | |
| QY | 2167 | CTTTG | GAAG | AGATAG | AG | ACTACT | TTG | TAG | CTA | AGAATCA | AGGTAC | AGTCTAC | CG | AGG | AGAA | | 2226 | | | |
| DB | 4148 | ATT | TG | CAAA | AGATAA | AG | ACTAC | CTTGT | TAG | CAAG | AAACG | CCG | CAAA | CGTCTAT | CGG | GTTC | 4207 | | | |
| QY | 2227 | TC | CTAT | TAC | CGA | ----- | CAAC | GAAC | CTATAT | CTCT | CTCTT | CTT | TG | CAAA | CTAC | GGCC | 2280 | | | |
| DB | 4208 | TG | TATAT | TATC | AG | ATGTG | AGCA | AGTTTG | ATG | ATCTCAC | GGT | TATTTAAT | GGG | CC | TAA | | 4267 | | | |
| QY | 2281 | TTG | TTCC | TGCT | CTAT | CTC | TAC | AG | ATTTCT | TGTT | CTCT | TTTTC | TG | CAAA | CTAC | GGCTA | 2340 | | | |
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| QY | 2341 | CAC | CCATAG | CGG | ATAAC | GAATG | AAACCA | AGTAT | CAACA | TATCC | TACTCT | TG | TAA | AGG | AG | | 2400 | | | |
| DB | 4328 | TTG | CCAC | ACG | GGCAACA | ATG | CAACG | TCCTAT | AC | AGCTAT | CTCTG | AACTG | GAAG | AGG | TTTC | | 4387 | | | |
| QY | 2401 | CTG | GGG | GAATG | ATGTT | TCG | TTTAG | TAATTC | CGT | TGGA | AG | AGCTCCG | ATTTG | CTTTAG | TATG | ATGA | 2460 | | | |
| DB | 4388 | TTG | GGG | TAA | TGATAC | CCCTG | G | GCTTAA | CTTTG | CT | TAG | CTAC | CT | TAT | CCG | GTATTTAG | 4447 | | | |
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| DB | 4508 | AGAT | G | ACTTTTAA | AGAACCA | CAC | AG | AG | CGCCGG | GCTTTG | AAAG | CAC | AG | CA | CTTCT | CTCA | | | | 4567 |

| | | | | |
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| QY | 2581 | TCITGGCTTACCTATCGGATCCGATTTTGATAGGAATCAGATGCCAAGATGCAACGTA | 2640 | |
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| QY | 2641 | CAATCTAACTCTTGGTTATATCTGTGGATCTTGTGTAGTAACCCCGACTGTACGACAAC | 2700 | |
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| QY | 2701 | ACTGCGAATTAGCGGTGATTTCTTGGAAAACTTTCGGTACGAAATTTGGCAAGACAAGCTTTT | 2760 | |
| Db | 4688 | ATTGGGATCAATGATGACGTTTCCTGGTTAAACCAAGCTACGAACTTCTGTAGACAAAGCTTT | 4747 | |
| QY | 2761 | AGTCCTTCGTGAGGAAACCAATTTTGGCTTTAACTCAAAATTTTGAAGCCTTTAGCCAAAT | 2820 | |
| Db | 4748 | CATAGTTTCGCGCGGGTAACCATATTTGCCCTTTAACTCTGGTGTTCAGATGTTTCAGTCAGTT | 4807 | |
| QY | 2821 | TTCTTTTGAATTCGTGGGTCACTCGCAATTACAAATGTAGACTTAGGACGAAAAATACCA | 2880 | |
| Db | 4808 | TGGTTTCGAATTCGAAGCTCTTCAAGAAATATAAGCTAGATCTTGGCGCTAAGGTCGC | 4867 | |
| QY | 2881 | ATTCTAA | 2887 | |
| Db | 4868 | GTCTAA | 4874 | |
| RESULT 12 | AE002192 | 12676 bp | DNA linear | BCT 30-MAY-2000 |
| LOCUS | Chlamydothila pneumoniae AR39, section 25 of 94 of the complete genome. | | | |
| ACCESSION | AE002192 | AE002161 | | |
| VERSION | AE002192.2 | GI:8163405 | | |
| KEYWORDS | | | | |
| SOURCE | Chlamydothila pneumoniae AR39 | | | |
| ORGANISM | Chlamydothila pneumoniae AR39 | | | |
| REFERENCE | Bacteria; Chlamydiales; Chlamydiales; Chlamydiales; Chlamydiales; Chlamydiales. | | | |
| AUTHORS | Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Unayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. | | | |
| TITLE | Genome sequences of Chlamydia trachomatis MOPn and Chlamydia pneumoniae AR39 | | | |
| JOURNAL | Nucleic Acids Res. 28 (6), 1397-1406 (2000) | | | |
| MEDLINE | 20150255 | | | |
| PUBMED | 10684935 | | | |
| REFERENCE | 2 (bases 1 to 12676) | | | |
| AUTHORS | Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Unayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. | | | |
| TITLE | Direct Submission | | | |
| JOURNAL | Submitted (01-MAR-2000) The Institute for Genomic Research, 9712 | | | |
| COMMENT | Medical Center Dr, Rockville, MD 20850, USA | | | |
| FEATURES | On Jun 1, 2000 this sequence version replaced gi:71892226. | | | |
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| KEYWORDS | | | |
| SOURCE | Chlamydomphila pneumoniae J138 | | |
| ORGANISM | Chlamydomphila pneumoniae J138 | | |
| REFERENCE | 1 | Shirai, M., Hirakawa, H., Ouchi, K., Tabuchi, M., Kishi, F., Kimoto, M., Takeuchi, A., Nishida, J., Shibata, K., Fujinaga, R., Yoneda, H., Matsushima, H., Tanaka, C., Furukawa, S., Miura, K., Nakazawa, A., Ishii, K., Shiba, T., Hattori, M., Kuhara, S. and Nakazawa, T. | |
| AUTHORS | | Comparison of outer membrane protein genes omp and pmp in the whole genome sequences of Chlamydia pneumoniae isolates from Japan and the United States | |
| TITLE | | J. Infect. Dis. 181 Suppl 3, S524-S527 (2000) | |
| JOURNAL | | 20298986 | |
| MEDLINE | | 10839753 | |
| PUBMED | | | |
| REFERENCE | 2 | Shirai, M., Hirakawa, H., Kimoto, M., Tabuchi, M., Kishi, F., Ouchi, K., Shiba, T., Ishii, K., Hattori, M., Kuhara, S. and Nakazawa, T. | |
| AUTHORS | | Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA | |
| TITLE | | Nucleic Acids Res. 28 (12), 2311-2314 (2000) | |
| JOURNAL | | 20330349 | |
| MEDLINE | | 10871362 | |
| PUBMED | | | |
| REFERENCE | 3 | (bases 1 to 300650) | |
| AUTHORS | | Shirai, M. | |
| TITLE | | Direct Submission | |
| JOURNAL | | Submitted (04-JUL-2000) Mutsunori Shirai, Yamaguchi University | |
| MEDLINE | | School of Medicine, Department of Microbiology; 1-1-1 | |
| PUBMED | | Minamikogushi, Ube, Yamaguchi 755-8505, Japan | |
| REFERENCE | | | |

(E-mail: mehiraipo.cc.yamaguchi-u.ac.jp, Tel: 81-836-22-2227, Fax: 81-836-22-2415)
 On or before Sep 15, 2000 this sequence version replaced
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FEATURES

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RESULT 14

AE001628/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

AE001628 10757 bp DNA linear BCT 01-DEC-2000
Chlamydia pneumoniae section 44 of 103 of the complete genome.

AE001628.1 GI:4376730

Chlamydia pneumoniae CWL029

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia

1 (bases 1 to 10757)

Kalmann, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R.W.,

Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.

Comparative genomes of Chlamydia pneumoniae and C. trachomatis

Nat. Genet. 21 (4), 385-389 (1999)

99206606

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RESULT 15
A81829
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DEFINITION Sequence 3 from Patent WO9858953.
ACCESSION A81829
VERSION A81829.1 GI:6731865
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 2815)


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Qy      2734  CGGTACGAATTTGGCAAGACAAAGCTTTAGTCCTTGTGTCAGGGAAACCAATTTTGCTTTAA  2793
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Search completed: December 16, 2003, 15:32:04
Job time : 10708 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 12:10:57 ; Search time 752 Seconds

(without alignments)
10769.035 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 3000

Sequence: 1 cgctctacacgtagaggt.....tggtttgctaaacacttc 3000

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 2775.8 | 92.5 | 2787 | 20 | AAx06820 |
| 4 | 2241 | 74.7 | 2241 | 24 | ABL91193 |
| 5 | 546.6 | 18.2 | 2781 | 24 | ABQ84775 |
| 6 | 546.6 | 18.2 | 2781 | 24 | ABQ78033 |
| 7 | 546.6 | 18.2 | 2781 | 25 | ABX99200 |
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| | | | | | Chlamydia pneumoniae |
| | | | | | Nucleotide sequence |
| | | | | | Chlamydia pneumoniae |
| | | | | | Chlamydia pneumoniae |
| | | | | | Chlamydia psittaci |
| | | | | | Chlamydia psittaci |
| | | | | | C. psittaci genome |
| | | | | | Chlamydia pneumoniae |

| | | | | | |
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| 9 | 530.2 | 17.7 | 2815 | 20 | AAx06817 |
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| 12 | 523 | 17.4 | 534 | 24 | ABL91192 |
| 13 | 522.2 | 17.4 | 2757 | 20 | AAx06821 |
| 14 | 518.2 | 17.3 | 2950 | 21 | AAx0851 |
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| 16 | 516.6 | 17.2 | 273254 | 21 | AAC81914 |
| 17 | 515.2 | 17.2 | 2784 | 21 | AAx0852 |
| 18 | 515 | 17.2 | 2787 | 20 | AAx06822 |
| 19 | 514 | 17.1 | 2793 | 20 | AAx06823 |
| 20 | 514 | 17.1 | 2793 | 24 | ABL91206 |
| 21 | 513.6 | 17.1 | 3000 | 21 | AAx0853 |
| 22 | 512.6 | 17.1 | 2950 | 21 | AAx0849 |
| 23 | 509.8 | 17.0 | 1230025 | 20 | AAx91990 |
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| 25 | 506 | 16.9 | 3000 | 20 | AAx06828 |
| 26 | 503.6 | 16.8 | 2811 | 24 | ABL91260 |
| 27 | 491.8 | 16.4 | 2790 | 21 | AAx0854 |
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| 29 | 459.4 | 15.6 | 2784 | 21 | AAx0850 |
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| 38 | 348.4 | 11.6 | 2520 | 24 | ABQ78016 |
| 39 | 348.4 | 11.6 | 2520 | 25 | ABX99183 |
| 40 | 345 | 11.5 | 2526 | 21 | AAx28691 |
| 41 | 345 | 11.5 | 2526 | 24 | ABL91253 |
| 42 | 340.2 | 11.3 | 2526 | 20 | AAx06819 |
| 43 | 289 | 9.6 | 1065 | 24 | ABL91191 |
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| 45 | 273.2 | 9.1 | 3052 | 20 | AAx06818 |

ALIGNMENTS

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| AC | AAA27021; |
| XX | |
| XX | |
| DT | 11-AUG-2000 (first entry) |
| XX | |
| DE | Chlamydia pneumoniae 98kD putative outer membrane protein gene. |
| XX | |
| KW | Chlamydia; antigen; vaccine; infection; outer membrane protein; ds. |
| XX | |
| OS | Chlamydia pneumoniae. |
| XX | |
| PH | Location/Qualifiers |
| FT | 101..2887 |
| FT | /*tag= a |
| FT | /product= "98kDa putative outer membrane protein" |
| XX | |
| PN | W0200026237-A2. |
| XX | |
| PD | 11-MAY-2000. |
| XX | |
| XX | 29-OCT-1999; 99WO-GB03579. |
| XX | |
| PR | 29-OCT-1998; 98US-0106070. |
| PR | 01-MAR-1999; 99US-0122066. |
| PR | 27-OCT-1999; 99US-0428122. |
| XX | |
| PA | (CONN-) CONNAUGHT LAB LTD. |
| XX | |

| | | | |
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| Qy | 1621 | AGAAACCAAAGCTACGTCACAAAAATCTGACCTTTATCTGGAAACCATCACTCTTTATTTGGACCC | 1680 |
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| Qy | 1681 | GACGGGCACGTTTTATGAAATCATAGTTTTAAGAAATCCTCAGTCCCTACGACATCTTTAGA | 1740 |
| Db | 1681 | GACGGGCACGTTTTATGAAATCATAGTTTTAAGAAATCCTCAGTCCCTACGACATCTTTAGA | 1740 |
| Qy | 1741 | GCTCAAAAGCTTCTGGAACTGTAAACAAGCACCGCAGTGACTCCAGATCCTATATAATGGGTGA | 1800 |
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| Qy | 1801 | GAAATTCATTTACGGCTATCAGGAACTTTGGGGCCCAATTTGTTGGGGGACAGGGGCTTC | 1860 |
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| Qy | 1861 | TACGACTGCAACCTTCAACTGCACTAAAACCTGGCTATATTCCTAATCCCAGGCGTATCGG | 1920 |
| Db | 1861 | TACGACTGCAACCTTCAACTGCACTAAAACCTGGCTATATTCCTAATCCCAGGCGTATCGG | 1920 |
| Qy | 1921 | CTCTTTAGTCCTTAATAGCTTTATGGAATGCAATTTATAGATATTAGCTCTCTCCATTAATCT | 1980 |
| Db | 1921 | CTCTTTAGTCCTTAATAGCTTTATGGAATGCAATTTATAGATATTAGCTCTCTCCATTAATCT | 1980 |
| Qy | 1981 | TATGGAGACTGCAAAACGAAGGGTTGCGGGGAGACCGTGTCTTTTGGTGTCTGGATTATC | 2040 |
| Db | 1981 | TATGGAGACTGCAAAACGAAGGGTTGCGGGGAGACCGTGTCTTTTGGTGTCTGGATTATC | 2040 |
| Qy | 2041 | TAACTTCTTCCATAAGGATAGTACAAAACACGACGCGGGTTTCGCCATTTGAGTGGCGG | 2100 |
| Db | 2041 | TAACTTCTTCCATAAGGATAGTACAAAACACGACGCGGGTTTCGCCATTTGAGTGGCGG | 2100 |
| Qy | 2101 | TTATGTCTATAGGAGAAACCTTACATACCTTGTTCAGATAAGATCTTAGTGTCTGCAATTTTG | 2160 |
| Db | 2101 | TTATGTCTATAGGAGAAACCTTACATACCTTGTTCAGATAAGATCTTAGTGTCTGCAATTTTG | 2160 |
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| Db | 2221 | AGGAACCTCTATTACCAGACACACGAAACCTATATCTCTCTCTCTTTGCGAAAACCTACGGCC | 2280 |
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| Db | 2281 | TTGTTTCGTTGTCTTATGTTCTCCTACAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCTA | 2340 |
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| Qy | 2401 | CTGGGGAAATGATAGTTTCGCTTTAGAAATTCGGTGGAGAGCTCCGATTTGCTTTAGATGA | 2460 |
| Db | 2401 | CTGGGGAAATGATAGTTTCGCTTTAGAAATTCGGTGGAGAGCTCCGATTTGCTTTAGATGA | 2460 |
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| Db | 2461 | AAGTGTCTTATTGAGCAGTACATGCCCTTCATGAAATTCAGTTTGTCTATGCACATCA | 2520 |
| Qy | 2521 | GGAAAGTTTTAAAGAACACGGGACAGAAAGCTCGTGAATTTGGAAGTAGCCGCTCTTGTA | 2580 |
| Db | 2521 | GGAAAGTTTTAAAGAACACGGGACAGAAAGCTCGTGAATTTGGAAGTAGCCGCTCTTGTA | 2580 |
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| Db | 2641 | CAATCTAACTCTTGGTTATAGTGGATCTTTGTTCCGTAGTAAACCCGACGTGTACGACAC | 2700 |
| Qy | 2701 | ACTGCGAATTAGCGGTGATTTCTTGGAAAAACCTTCCTGGTACGAATTTGGCAAGACAAGCTTT | 2760 |

| | | | | | | |
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| QY | 2761 | AGTCCTTCGTCAGGGAACCAATTTTGGCTTAACTCAAAATTTTGAAGCCTTTAGCCAAAT | 2820 | | | |
| Db | 2761 | AGTCCTTCGTCAGGGAACCAATTTTGGCTTAACTCAAAATTTTGAAGCCTTTAGCCAAAT | 2820 | | | |
| QY | 2821 | TTCTTTTGAATTCGCTGGTGCATCTCGCAATTTACAATGTAGACTTAGAGCMAAATACCA | 2880 | | | |
| Db | 2821 | TTCTTTTGAATTCGCTGGTGCATCTCGCAATTTACAATGTAGACTTAGAGCMAAATACCA | 2880 | | | |
| QY | 2881 | ATTCTAATGCTTAGCTTTGGTAAAGAGCTCCATACATCGAAGGGAAGAGCTTTTAAAG | 2940 | | | |
| Db | 2881 | ATTCTAATGCTTAGCTTTGGTAAAGAGCTCCATACATCGAAGGGAAGAGCTTTTAAAG | 2940 | | | |
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| AC | AAx91990; | | | | | |
| XX | | | | | | |
| DT | 13-SEP-1999 (first entry) | | | | | |
| XX | | | | | | |
| DE | Nucleotide sequence of the complete genome of Chlamydia pneumoniae. | | | | | |
| XX | | | | | | |
| KW | Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; | | | | | |
| KW | sinusitis; purulent otitis media; erythema nodosum; pharyngitis; | | | | | |
| KW | vaccine; neutralising epitope; ss. | | | | | |
| OS | Chlamydia pneumoniae. | | | | | |
| XX | | | | | | |
| PN | WO9927105-A2. | | | | | |
| XX | | | | | | |
| PD | 03-JUN-1999. | | | | | |
| XX | | | | | | |
| PF | 20-NOV-1998; 98WO-IB01890. | | | | | |
| XX | | | | | | |
| PR | 04-NOV-1998; 98US-0107078. | | | | | |
| PR | 21-NOV-1997; 97FR-0014673. | | | | | |
| PA | (GEST) GENSET. | | | | | |
| XX | | | | | | |
| PI | Griffais R; | | | | | |
| XX | | | | | | |
| DR | WPI; 1999-357842/30. | | | | | |
| XX | | | | | | |
| PT | Genome sequence of Chlamydia pneumoniae | | | | | |
| XX | | | | | | |
| PS | Claim 1; Page 291-611; 1912pp; English.. | | | | | |
| XX | | | | | | |
| CC | The present sequence represents the complete genome of Chlamydia | | | | | |
| CC | pneumoniae, and encodes proteins AAy34584-Y35879. C. pneumoniae causes | | | | | |
| CC | respiratory disease such as pneumonia and bronchitis and is thought | | | | | |
| CC | to be a contributing factor in heart disease, sarcoidosis, sinusitis, | | | | | |
| CC | purulent otitis media, erythema nodosum or pharyngitis. The polypeptides | | | | | |
| CC | encoded by the open reading frames of the C. pneumoniae genome (see | | | | | |
| CC | AAy34584-Y35879) can be used in immunogenic compositions as vaccines. | | | | | |
| CC | Vectors containing C. pneumoniae nucleotide sequences can also be | | | | | |
| CC | used as immunogenic compositions, especially where the vector directs | | | | | |
| CC | the expression of a neutralising epitope of C. pneumoniae. | | | | | |
| XX | | | | | | |
| SQ | Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other; | | | | | |
| Query Match | | | | | | |
| Best Local Similarity 99.2%; Score 2975.4; DB 20; Length 1230025; | | | | | | |
| Matches 2998; Conservative 0; Mismatches 1; Indels 2; Gaps 2; | | | | | | |
| QY | 1 CGCTCTTACTAGTAGAGGTTGAGTGAATTTCTGTGACTGTTTCTCTATTGTGTATCT 60 | | | | | |

| | | | |
|----|-------|---|-------|
| Db | 31658 | CGCTCTACCTAGTAGAGGTGAGTGAATTCITGACTTGTTCTCTATTTGGTGAATCT | 31717 |
| Qy | 61 | CTTAAATATTAATCAAAATCAAAAGTATATATTTTACAATGAAGTCTCTTTTCCCCAA | 120 |
| Db | 31718 | CTTAAATATTAATCAAAATCAAAAGTATATATTTTACAATGAAGTCTCTTTTCCCCAA | 31777 |
| Qy | 121 | GTTTGATATTTTCTACATTTGCTATTTTCCCTTTGTCTATGATTTGCTACCGAGACAGTTTT | 180 |
| Db | 31778 | GTTTGATATTTTCTACATTTGCTATTTTCCCTTTGTCTATGATTTGCTACCGAGACAGTTTT | 31837 |
| Qy | 181 | GGATTCAAGTCGAGTTTCAGATGGGAATAAAATGGTAAATTTTTCAGTTTCGTCGAGAGTCA | 240 |
| Db | 31838 | GGATTCAAGTCGAGTTTCAGATGGGAATAAAATGGTAAATTTTTCAGTTTCGTCGAGAGTCA | 31897 |
| Qy | 241 | GGAGATGCTGGAACTACCTATTTTAAAGGAAATGTCACTCTAGAAAATATTCCTGG | 300 |
| Db | 31898 | GGAGATGCTGGAACTACCTATTTTAAAGGAAATGTCACTCTAGAAAATATTCCTGG | 31957 |
| Qy | 301 | AACAGGCACAGCAATCACAAAAGCTGTTTAAACAACACTAAGGGCGATTTGACTTTTAC | 360 |
| Db | 31958 | AACAGGCACAGCAATCACAAAAGCTGTTTAAACAACACTAAGGGCGATTTGACTTTTAC | 32017 |
| Qy | 361 | AGGTAACGGGAACCTCTCTATTTGTTTCAAACGGTGGATGCAGGACTGTAGCAGGGCTGC | 420 |
| Db | 32018 | AGGTAACGGGAACCTCTCTATTTGTTTCAAACGGTGGATGCAGGACTGTAGCAGGGCTGC | 32077 |
| Qy | 421 | TGTTAAACAGCAGCGTGGTAGATAAAATCTACCACTTTATAGGGTTTCTTCGCTATCTTT | 480 |
| Db | 32078 | TGTTAAACAGCAGCGTGGTAGATAAAATCTACCACTTTATAGGGTTTCTTCGCTATCTTT | 32137 |
| Qy | 481 | TATTTGGCTCTCTGGAGTTTCGATTAACCTACCGCAAGAGCCGTTAGCTGCTCTACGGG | 540 |
| Db | 32138 | TATTTGGCTCTCTGGAGTTTCGATTAACCTACCGCAAGAGCCGTTAGCTGCTCTACGGG | 32197 |
| Qy | 541 | TAGCTTGAGTTTGACAAAAATGTCAGTTTGCTCTTCAGCAAAAATCTTTTCAACGGATAA | 600 |
| Db | 32198 | TAGCTTGAGTTTGAC-AAAAATGTCAGTTTGCTCTTCAGCAAAAATCTTTTCAACGGATAA | 32256 |
| Qy | 601 | TGGCGGTGTATCACCGCAAAAATCTCTTTTCAATTAACAGGAGCTACAATGTCTGT | 660 |
| Db | 32257 | TGGCGGTGTATCACCGCAAAAATCTCTTTTCAATTAACAGGAGCTACAATGTCTGT | 32316 |
| Qy | 661 | TTCTGAAAATACCTCTCTCAAGAAAGCGGAGCCATTTCAGACTTCGATGCCCTTACCAT | 720 |
| Db | 32317 | TTCTGAAAATACCTCTCTCAAGAAAGCGGAGCCATTTCAGACTTCGATGCCCTTACCAT | 32376 |
| Qy | 721 | TACTGAAAACCAAGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGATTCGAGCTGC | 780 |
| Db | 32377 | TACTGAAAACCAAGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGATTCGAGCTGC | 32436 |
| Qy | 781 | AATTTTTCAGAGAGCTCGGTGCTATTTCTTAATAATGCTAAAGTTTCCTTTATTCACAA | 840 |
| Db | 32437 | AATTTTTCAGAGAGCTCGGTGCTATTTCTTAATAATGCTAAAGTTTCCTTTATTCACAA | 32496 |
| Qy | 841 | TAAAGTTCACAGGAGGAGCTCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGC | 900 |
| Db | 32497 | TAAAGTTCACAGGAGGAGCTCTCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGC | 32556 |
| Qy | 901 | TTATAAACTAGTACAGATACTAAGGTCACTTCAGTCACTTGGAAATCAGATGTTACTCTTCAG | 960 |
| Db | 32557 | TTATAAACTAGTACAGATACTAAGGTCACTTCAGTCACTTGGAAATCAGATGTTACTCTTCAG | 32616 |
| Qy | 961 | CAACAATATACACAACAGCGGGAGAGCTATCTATGTGMAAAAGCTCGAATCGGCTTC | 1020 |
| Db | 32617 | CAACAATATACACAACAGCGGGAGAGCTATCTATGTGMAAAAGCTCGAATCGGCTTC | 32676 |
| Qy | 1021 | CGAGGACTTACCTCTTACGATAGAAATAGTGTCAATGGAGGTACAGCTCCCTAAAGGTGG | 1080 |
| Db | 32677 | CGAGGACTTACCTCTTACGATAGAAATAGTGTCAATGGAGGTACAGCTCCCTAAAGGTGG | 32736 |
| Qy | 1081 | AGCCATAGCTATCGAAGATAGTGGGAAATGAGTTTATCCGCCGATAGTGGTGACATTTGT | 1140 |

| | | | |
|----|-------|---|-------|
| Db | 32737 | AGCCATAGCTATCGAAGATAGTGGGAAATGAGTTTATCCGCCGATAGTGGTGACATTTGT | 32796 |
| Qy | 1141 | CTTTTTPAGGAAATACAGTCACTTCTACTACTCTCTGGACGAATAGAAAGTAGTATCCACTT | 1200 |
| Db | 32797 | CTTTTTPAGGAAATACAGTCACTTCTACTACTCTCTGGACGAATAGAAAGTAGTATCCACTT | 32856 |
| Qy | 1201 | AGAAACGAGTCAAAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAGCCATCTACTTTCTA | 1260 |
| Db | 32857 | AGAAACGAGTCAAAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAGCCATCTACTTTCTA | 32916 |
| Qy | 1261 | TGATCCCATTAATCTACAGGATCATCCACAACAGTTACAGATGCTTTAAAGTTTAAAGAGAC | 1320 |
| Db | 32917 | TGATCCCATTAATCTACAGGATCATCCACAACAGTTACAGATGCTTTAAAGTTTAAAGAGAC | 32976 |
| Qy | 1321 | TCCGCGAGATTTCTGCATACAATATACAGGGAACATCATCTTTCACAGGAGAAAAGTTATC | 1380 |
| Db | 32977 | TCCGCGAGATTTCTGCATACAATATACAGGGAACATCATCTTTCACAGGAGAAAAGTTATC | 33036 |
| Qy | 1381 | AGAGACAGAGGGCGCGAGATTTCTAAANAATCTTACTTTCGAAGCTACTACAGCTGTAACTCT | 1440 |
| Db | 33037 | AGAGACAGAGGGCGCGAGATTTCTAAANAATCTTACTTTCGAAGCTACTACAGCTGTAACTCT | 33096 |
| Qy | 1441 | TTTTCAGGAGTACTCTATCTTTTAAACAATGAGTCTCTGAGACTCTGAGCAATTCACITCA | 1500 |
| Db | 33097 | TTTTCAGGAGTACTCTATCTTTTAAACAATGAGTCTCTGAGACTCTGAGCAATTCACITCA | 33156 |
| Qy | 1501 | ACAGGCGAGATTTCTCGTCTCGAAAATGAGCTAGGAACTACTCTAGAACCTCTGTGACTAG | 1560 |
| Db | 33157 | ACAGGCGAGATTTCTCGTCTCGAAAATGAGCTAGGAACTACTCTAGAACCTCTGTGACTAG | 33216 |
| Qy | 1561 | CACCAATAACAATTTGGTCAATTAACATCAGTTCTTATAGACGGTGCAGGCAAGCAAAAT | 1620 |
| Db | 33217 | CACCAATAACAATTTGGTCAATTAACATCAGTTCTTATAGACGGTGCAGGCAAGCAAAAT | 33276 |
| Qy | 1621 | AGAAACCAAGCTACGTCAAAANAATCTGACTTTATCTGAAACCATCATTTTATTCGACCC | 1680 |
| Db | 33277 | AGAAACCAAGCTACGTCAAAANAATCTGACTTTATCTGAAACCATCATTTTATTCGACCC | 33336 |
| Qy | 1681 | GACGCGACGTTTTATGAAAATCATAGTTTAAAGAAATCTCAGTCTCTACGACATCTTAGA | 1740 |
| Db | 33337 | GACGCGACGTTTTATGAAAATCATAGTTTAAAGAAATCTCAGTCTCTACGACATCTTAGA | 33396 |
| Qy | 1741 | GCTCAAAAGCTTCGGAACGTGTAACAGCACCGCAGTACTCCAGATCTCTAATGGGTGA | 1800 |
| Db | 33397 | GCTCAAAAGCTTCGGAACGTGTAACAGCACCGCAGTACTCCAGATCTCTAATGGGTGA | 33456 |
| Qy | 1801 | GAAATTCATTAACGCTATCAGGGAACCTTGGGGGCCAAATTTGTTGGGGGACAGGGGCTTC | 1860 |
| Db | 33457 | GAAATTCATTAACGCTATCAGGGAACCTTGGGGGCCAAATTTGTTGGGGGACAGGGGCTTC | 33516 |
| Qy | 1861 | TACGACTGCAACCTTCAACTGGACTTAAACCTGGCTATATTCCTAATCCGAGCGTATCGG | 1920 |
| Db | 33517 | TACGACTGCAACCTTCAACTGGACTTAAACCTGGCTATATTCCTAATCCGAGCGTATCGG | 33576 |
| Qy | 1921 | CTCTTTAGTCCCTATAGCTTATGGAATGCATTTTATAGATTTAGCTCTCTCCATTTATCT | 1980 |
| Db | 33577 | CTCTTTAGTCCCTATAGCTTATGGAATGCATTTTATAGATTTAGCTCTCTCCATTTATCT | 33636 |
| Qy | 1981 | TATGGAGACTGCAAAACGAGGGTTTCAGGAGACCGTCTGTTTTTGGTGTCTGCTGGATTATC | 2040 |
| Db | 33637 | TATGGAGACTGCAAAACGAGGGTTTCAGGAGACCGTCTGTTTTTGGTGTCTGCTGGATTATC | 33696 |
| Qy | 2041 | TAACTCTTCCATAAGGATAGTACAAAACAGCACGCGGGTTTCGCCATTTTGGTGGGG | 2100 |
| Db | 33697 | TAACTCTTCCATAAGGATAGTACAAAACAGCACGCGGGTTTCGCCATTTTGGTGGGG | 33756 |
| Qy | 2101 | TTATGCTCATAGAGAAACCTACATCTTGTTCAGATAGATTTCTTAGTGTGCAATTTTG | 2160 |
| Db | 33757 | TTATGCTCATAGAGAAACCTACATCTTGTTCAGATAGATTTCTTAGTGTGCAATTTTG | 33816 |
| Qy | 2161 | TCAGCTCTTTTGGAGAGATAGAGACTCTTTTGTAGCTAAGATC-AAGGTACAGTCTAGG | 2219 |
| Db | 33817 | TCAGCTCTTTTGGAGAGATAGAGACTCTTTTGTAGCTAAGATC-AAGGTACAGTCTAGG | 33876 |

Db 301 GGGACGTAGCAGGGGCTGCTGTTAAACAGCAGCGGTAGATAAAATCTACACGTTTATA 360
Qy 461 GGGTTTCTTCGCTATCTTTTATGCTCTCTGCGAGTTTCGATACCTACCGGCAAGGA 520
Db 361 GGGTTTCTTCGCTATCTTTTATGCTCTCTGCGAGTTTCGATACCTACCGGCAAGGA 420
Qy 521 GCGTTAGCTGCTTACCGGTAGCTTGGTTTGCACAAAAATSTCAGTTTGTCTTCAGC 580
Db 421 GCGTTAGCTGCTTACCGGTAGCTTGAAGTTTGACAAAAATGTTCAGTTTGTCTTCAGC 480
Qy 581 AAAAACTTTTCAACGATTAATGGCGGTCTATCAACGCAAAACTCTTTTCAATTAACAGG 640
Db 481 AAAAACTTTTCAACGATTAATGGCGGTCTATCAACGCAAAACTCTTTTCAATTAACAGG 540
Qy 641 ACTACAAATGTCAGCTCTGTTTCTGAAATACCTCTCAAGAAAGGGGAGCCATTTCAG 700
Db 541 ACTACAAATGTCAGCTCTGTTTCTGAAATACCTCTCAAGAAAGGGGAGCCATTTCAG 600
Qy 701 ACTTCGATGCCCTTACCAATTAAGTGAACCAAGGGGAAGTCTCTTTTCTGACAAATCT 760
Db 601 ACTTCGATGCCCTTACCAATTAAGTGAACCAAGGGGAAGTCTCTTTTCTGACAAATCT 660
Qy 761 TCTTCGATTTCTGAGCTCAATTTTACAGAGCTCGGTGACTATTTCTAATAATGCT 820
Db 661 TCTTCGATTTCTGAGCTCAATTTTACAGAGCTCGGTGACTATTTCTAATAATGCT 720
Qy 821 AAAGTTTCCCTTTATTGACAAATAGTTCACAGAGCGAGCTCTCAACACCGGGGATG 880
Db 721 AAAGTTTCCCTTTATTGACAAATAGTTCACAGAGCGAGCTCTCAACACCGGGGATG 780
Qy 881 TCAGGAGGTGCTATCTGCTTATATAAACTAGTACAGATACCTAAGTCAACCTCTACTGGA 940
Db 781 TCAGGAGGTGCTATCTGCTTATATAAACTAGTACAGATACCTAAGTCAACCTCTACTGGA 840
Qy 941 AATCAGATGTTACTCTTTCAGCAACAATATCATGACACAGCGGGAGGACTATCTATGTG 1000
Db 841 AATCAGATGTTACTCTTTCAGCAACAATATCATGACACAGCGGGAGGACTATCTATGTG 900
Qy 1001 AAAAACTCGAATGCTTCGAGGACTTACCTATTCAGTAAATAGTCTCAATGGA 1060
Db 901 AAAAACTCGAATGCTTCGAGGACTTACCTATTCAGTAAATAGTCTCAATGGA 960
Qy 1061 GGTACAGCTCCTAAAGTGAGCCTATGCTATCGAAGATAGTGGGAATGAGTTTATCC 1120
Db 961 GGTACAGCTCCTAAAGTGAGCCTATGCTATCGAAGATAGTGGGAATGAGTTTATCC 1020
Qy 1121 GCGGATAGTGGTGACATGCTTTTATGGAATACAGTCACTTCTACTACTCTCTGGGAGC 1180
Db 1021 GCGGATAGTGGTGACATGCTTTTATGGAATACAGTCACTTCTACTACTCTCTGGGAGC 1080
Qy 1181 AATAGAGTATGTTTACGACTTAGGAACGAGTGCAAGATACAGCTTTGCTGCTGCT 1240
Db 1081 AATAGAGTATGTTTACGACTTAGGAACGAGTGCAAGATACAGCTTTGCTGCTGCT 1140
Qy 1241 GGTAGAGCCATCTACTTCTATGATCCCAATACCTACAGGATCATCCACACAGTTACAGAT 1300
Db 1141 GGTAGAGCCATCTACTTCTATGATCCCAATACCTACAGGATCATCCACACAGTTACAGAT 1200
Qy 1301 GTCTTAAAGTTAATGAGCTCCGAGATCTGCACTACATATATACAGGAAACATCATC 1360
Db 1201 GTCTTAAAGTTAATGAGCTCCGAGATCTGCACTACATATATACAGGAAACATCATC 1260
Qy 1361 TTCAACAGGAAAGTTTATCAGACACAGGCGCCAGATTTCTAAAAATCTTACTTCGAAG 1420
Db 1261 TTCAACAGGAAAGTTTATCAGACACAGGCGCCAGATTTCTAAAAATCTTACTTCGAAG 1320
Qy 1421 CTACTACAGCTGPAATCTCTTTCAGGAGGTACTCTATCTTTTAAAAATGAGGAGTCTG 1480
Db 1321 CTACTACAGCTGPAATCTCTTTCAGGAGGTACTCTATCTTTTAAAAATGAGGAGTCTG 1380
Qy 1481 CAGACTCAGGATTTCACTCAACAGGAGATTTCTGCTCGAAATGAGGAGTCACT 1540

Db 1381 CAGACTCAGGCAATTCACACAGGAGATTTCTGCTCGAAATGAGCGTAGGAATCTACT 1440
Qy 1541 CTAGAACCTGCTGATACTAGCACCAATAAATTTGGTCAATTAACATCAGTTTCTTAGAC 1600
Db 1441 CTAGAACCTGCTGATACTAGCACCAATAAATTTGGTCAATTAACATCAGTTTCTTAGAC 1500
Qy 1601 GGTGCAAGAGGCAAAAAATAGAAACCAAGCTACGTCAAAAAATCTGACTTTATCTGA 1660
Db 1501 GGTGCAAGAGGCAAAAAATAGAAACCAAGCTACGTCAAAAAATCTGACTTTATCTGA 1560
Qy 1661 ACCATCAGCTTTATGACCGCGAGCGGCTTTTATGAAAAATCATAGTTTAAAGAAATCT 1720
Db 1561 ACCATCAGCTTTATGACCGCGAGCGGCTTTTATGAAAAATCATAGTTTAAAGAAATCT 1620
Qy 1721 CAGTCTTACGACATCTTAGAGCTCAAAGCTTCTGGAACCTGTAAACAGCACCGCAGTACT 1780
Db 1621 CAGTCTTACGACATCTTAGAGCTCAAAGCTTCTGGAACCTGTAAACAGCACCGCAGTACT 1680
Qy 1781 CCAGATCCTTAATGGTGAGAAATTCATTAAGGCTATCAGGAACTTTGGGGCCCAATT 1840
Db 1681 CCAGATCCTTAATGGTGAGAAATTCATTAAGGCTATCAGGAACTTTGGGGCCCAATT 1740
Qy 1841 GTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATT 1900
Db 1741 GTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATT 1800
Qy 1901 CTTAATCCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTATGAAATGCATTTATAGAT 1960
Db 1801 CTTAATCCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTATGAAATGCATTTATAGAT 1860
Qy 1961 ATTAGCTCTCTCATTTATTTAGGAGCTTCAACAGAGGGTTGCAGGAGACCGCTGCT 2020
Db 1861 ATTAGCTCTCTCATTTATTTAGGAGCTTCAACAGAGGGTTGCAGGAGACCGCTGCT 1920
Qy 2021 TTTTGGTGTGCTGGAATATCTAACTTCTTCCATTAAGGATAGTACAAAAACAGACGCGGG 2080
Db 1921 TTTTGGTGTGCTGGAATATCTAACTTCTTCCATTAAGGATAGTACAAAAACAGACGCGGG 1980
Qy 2081 TTTCCGCAATTTAGTGCGGTTATGTCATAGGAGGAAACCTACATACTTTGTCAGATAAG 2140
Db 1981 TTTCCGCAATTTAGTGCGGTTATGTCATAGGAGGAAACCTACATACTTTGTCAGATAAG 2040
Qy 2141 ATTCTTAGTGTGCTGCAATTTCTCAGCTCTTTTGAAGAGATAGAGACTTCTTTGAGCTAAG 2200
Db 2041 ATTCTTAGTGTGCTGCAATTTCTCAGCTCTTTTGAAGAGATAGAGACTTCTTTGAGCTAAG 2100
Qy 2201 AATCAAGGTACAGTCTACGAGGAACTCTCTATTAACAGCAACAGAAACCTATATCTCT 2260
Db 2101 AATCAAGGTACAGTCTACGAGGAACTCTCTATTAACAGCAACAGAAACCTATATCTCT 2160
Qy 2261 CTTCTTTGCAAACTACGCGCTTGTTCGTTGCTTATGTTCTTCTTACAGAGATTTCTGTTCTC 2320
Db 2161 CTTCTTTGCAAACTACGCGCTTGTTCGTTGCTTATGTTCTTCTTACAGAGATTTCTGTTCTC 2220
Qy 2321 TTTTCAGGAAACCTTAGCTACACCCATACCGATAACGATCTGAAACCAAGTATACAA 2380
Db 2221 TTTTCAGGAAACCTTAGCTACACCCATACCGATAACGATCTGAAACCAAGTATACAA 2280
Qy 2381 TATCCTACTGTAAAGGAAGCTGGGGAATGATAGTTTTCGCTTTTGAATTTGGTGGAAGA 2440
Db 2281 TATCCTACTGTAAAGGAAGCTGGGGAATGATAGTTTTCGCTTTTGAATTTGGTGGAAGA 2340
Qy 2441 GCTCCGATTTGCTTAGATGAAGTGTCTTATTTGAGCAGTACATGCTTCTCATGAAATTTG 2500
Db 2341 GCTCCGATTTGCTTAGATGAAGTGTCTTATTTGAGCAGTACATGCTTCTCATGAAATTTG 2400
Qy 2501 CAGTTTCTCTATGCACTCAGGAGGTTTAAAGAACAGGAGACAGAGCTCTGTAATTT 2560
Db 2401 CAGTTTCTCTATGCACTCAGGAGGTTTAAAGAACAGGAGACAGAGCTCTGTAATTT 2460
Qy 2561 GGAAGTACGCGCTCTGTTGAATCTTTCCTTACCTATCGGATCGGATTTGATAAGGAATCA 2620
Db 2461 GGAAGTACGCGCTCTGTTGAATCTTTCCTTACCTATCGGATCGGATTTGATAAGGAATCA 2520

QY 2621 GACTGCCAAGATGCAACGACATCAATTAATCTCTGCTTATAGTGTGATCTTGTTCGTAGT 2690
 DB |||||
 QY 2521 GACTGCCAAGATGCAACGACATCAATTAATCTCTGCTTATAGTGTGATCTTGTTCGTAGT 2580
 DB |||||
 QY 2681 AACCCGACTGTACGACAACTGCAATAGCGGTGATCTTGTGAAAACCTTCGCTACG 2740
 DB |||||
 QY 2581 AACCCGACTGTACGACAACTGCAATAGCGGTGATCTTGTGAAAACCTTCGCTACG 2640
 DB |||||
 QY 2741 AATTGGCAAGCAAGCTTTAGTCTCTGCTGAGGGAACCAATTTTGTCTTAACTCAAT 2800
 DB |||||
 QY 2641 AATTGGCAAGCAAGCTTTAGTCTCTGCTGAGGGAACCAATTTTGTCTTAACTCAAT 2700
 DB |||||
 QY 2801 TTGAAGCCTTTAGCAATTTCTTTGAATTCGCTGGGTCAATCTGCAATACAAATGA 2860
 DB |||||
 QY 2701 TTGAAGCCTTTAGCAATTTCTTTGAATTCGCTGGGTCAATCTGCAATACAAATGA 2760
 DB |||||
 QY 2861 GACTTAGGAGCAAAATACCAATCTAA 2887
 DB |||||
 QY 2761 GACTTAGGAGCAAAATACCAATCTAA 2787
 DB |||||

RESULT 4

ABL91193
 ID ABL91193 standard; DNA; 2241 BP.

XX ABL91193;

XX 29-JUL-2002 (first entry)

DE Chlamydia pneumoniae cp0015 ORF DNA, SEQ ID NO:20.

XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
 KW human respiratory disease; cardiovascular disease; atherosclerosis;
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
 KW strain CWL029; open reading frame; ORF; gene; ds.
 XX Chlamydia pneumoniae.

XX Key Location/Qualifiers

FF 1..2241

FT CDS /*tag= a

FT /product= "cp0015"

XX WO200202606-A2.

XX 10-JAN-2002.

XX 03-JUL-2001; 2001WO-IB01445.

XX 03-JUL-2000; 2000GB-0016363.

XX 11-JUL-2000; 2000GB-0017047.

XX 21-JUL-2000; 2000GB-0017983.

XX 07-AUG-2000; 2000GB-0019368.

XX 18-AUG-2000; 2000GB-0020440.

XX 14-SEP-2000; 2000GB-0022583.

XX 10-NOV-2000; 2000GB-0027549.

XX 22-DEC-2000; 2000GB-0031706.

XX (CHIR-) CHIRON SPA.

PA Ratti G, Grandi G;

XX WPI; 2002-154726/20.

XX N-PSDB; ABB90535.

XX Novel Chlamydia pneumoniae protein useful in the manufacture of a

PT medicament for treatment or prevention of infection due to Chlamydia,

PT preferably Chlamydia pneumoniae, and for diagnostic purposes -

XX Claim 5; Page 50; 364pp; English.

XX

CC Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is
 CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
 CC the invention.

XX Sequence 2241 BP; 660 A; 475 C; 478 G; 628 T; 0 other;

Query Match 74.7%; Score 2241; DB 24; Length 2241;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 ATGTCAGCTCTGTTTCTGAAAATACCTCTCTCAAGAAAGCGGAGCCATTTCAGACTTCC 706
 DB |||||
 QY 707 GATGCCCTTACCATTACTCGAAAACCAAGGGGAAGTCTCTTTTCTGCAATACTTCTTCG 766
 DB |||||
 QY 61 GATGCCCTTACCATTACTCGAAAACCAAGGGGAAGTCTCTTTTCTGCAATACTTCTTCG 120
 QY 767 GATCTGGAGCTGCAATTTTTCAGAAAGCTCGGTGACTATTTCTTAATAAGCTAAAGTT 826
 DB |||||
 QY 121 GATCTGGAGCTGCAATTTTTCAGAAAGCTCGGTGACTATTTCTTAATAAGCTAAAGTT 180
 QY 827 TCCTTTATTTGACAATAAGTTCACAGAGCGAGCTCTCTCAACACGGGGATATGTCAGA 886
 DB |||||
 QY 181 TCCTTTATTTGACAATAAGTTCACAGAGCGAGCTCTCTCAACACGGGGATATGTCAGA 240
 QY 887 GGTGCTATCTGTGCTTTATAAACTAGTACAGATCTAAGGTCACTTCACTGGAATCAG 946
 DB |||||
 QY 241 GGTGCTATCTGTGCTTTATAAACTAGTACAGATCTAAGGTCACTTCACTGGAATCAG 300
 QY 947 ATGTTACTCTTCAGCAACAAATACATCGCAACAGCGGGAGGAGCTATCTATGTGAAAAG 1006
 DB |||||
 QY 301 ATGTTACTCTTCAGCAACAAATACATCGCAACAGCGGGAGGAGCTATCTATGTGAAAAG 360
 QY 1007 CTCGAACTGGCTTCCGGAGGAGCTTACCTTATTCAGTAGAAATAGTGTCAATGGAGGTACA 1066
 DB |||||
 QY 361 CTCGAACTGGCTTCCGGAGGAGCTTACCTTATTCAGTAGAAATAGTGTCAATGGAGGTACA 420
 QY 1067 GCTCCTTAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATGAGTTTATCCGCCGAT 1126
 DB |||||
 QY 421 GCTCCTTAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATGAGTTTATCCGCCGAT 480
 QY 1127 AGTGGTGACATTTCTTTTATAGGGAATACAGTCACTTCTACTCTCTGGGACGAATAGA 1186
 DB |||||
 QY 481 AGTGGTGACATTTCTTTTATAGGGAATACAGTCACTTCTACTCTCTGGGACGAATAGA 540
 QY 1187 AGTAGTATCGACTTAGGAACGAGTGCAGAGATGCAAGATGACAGCTTTGCGTTCTGCTGTGAGA 1246
 DB |||||
 QY 541 AGTAGTATCGACTTAGGAACGAGTGCAGAGATGCAAGATGACAGCTTTGCGTTCTGCTGTGAGA 600
 QY 1247 GCCATCTACTTCTATGATCCCATACACAGATCATCCACACAGTTTACAGATGCTCTTA 1306
 DB |||||
 QY 601 GCCATCTACTTCTATGATCCCATACACAGATCATCCACACAGTTTACAGATGCTCTTA 660
 QY 1307 AAAGTTAATGAGACTCCGGCAGATTTCTGCACCTACATAATACAGGGAACATCTTTCACA 1366
 DB |||||
 QY 661 AAAGTTAATGAGACTCCGGCAGATTTCTGCACCTACATAATACAGGGAACATCTTTCACA 720
 QY 1367 GGAGAAAGTTATCAGAGACAGAGCCCGCAGATTTCTAATAATCTTCTTCGAAGTACTTA 1426

CC animal against Chlamydia psittaci comprising at least one polynucleotide
 CC (Ia) having a C. psittaci sequence, or at least one C. psittaci antigen
 CC (Ib), and a carrier. (Ia) and (Ib) have antibacterial activity. (I) is
 CC useful for the immunisation of a bovine. The present sequence encodes a
 CC C. psittaci antigen from the present invention.
 XX
 SQ Sequence 2781 BP; 818 A; 555 C; 610 G; 798 T; 0 other;

Query Match 18.2%; Score 546.6; DB 24; Length 2781;
 Best Local Similarity 53.7%; Pred. No. 4.2e-141; Indels 63; Gaps 10;
 Matches 1390; Conservative 0; Mismatches 1134;

328 TTTTAAACAACTAAGGCGGATTTGACTTTCACAGGTAACGGGAATCTCTATTGTCCA 387
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

388 AACGCTGATCAGGAGCTAGCAGGGGCTGCTGTTTAAACAGCAGCTGTGATTAATC 447
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

291 GAACGGAATCCGAGCTAATCC---TGCAGGAATTAACGTTAACACTCCCGATAGAT 347
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

448 TACCACGTTTATAGGGTTCCTTCGCTATCTTTTATTCGCTCTCTCGAAGTTGATAAC 507
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

348 TCTTAAGCTGACAGATTTTCTAAGTTGAGCTTTTAAAGGAATGCCATCTTCTAGTGA 407
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

508 TACCGGAAAGAGCGCTAGCTCTCTACGGGTAGCTTGAAGTTTGACAAAATGTCAG 567
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

408 TACTGGAAGAGGGG---TATGAATCCGGAGGAGCATTAACCTTAGCGAATATGCCAG 464
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

568 TTTGCTCTTCAGCAAAAATTTTCAACGGAATAATGGGGTGTCTATCACCCGCAAAAATCT 627
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

465 TATTCTGTTGATCAGAACTATTCGGTGAGAAATGGTGAGGCCATCTCTTGCAGAGCTTT 524
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

628 TTCATTAACAGGACTCAATGTGAGCTCTGTTTCTGAAATAATCTCTCTCAAGAAAGG 687
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

525 TTTCTAAACCGGCTCGAGCAAGAAATCAGCTTCCACCACTAATCTTACTGCGAAAAGG 584
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

688 CGGAGCCATTCAGACTCCGATGCCCTTACCATTACTGGAACCAAGGGGAAGTCTCTTT 747
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

585 TGGAGCAATTCGCTACGGGAATAGCTCATCTTTTCGGAACAACAGGACACATCAGATT 644
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

748 TTTGACAAATATCTTTCGGGATCTGGAGCTGCAATTTTACAGAGCTCTGGTACTAT 807
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

645 TTTCTGGGAACACTGCTGTGAATTTCTGGGGAGAGAGTATATTTCAGAACTTCTATGACGAT 704
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

808 TTTCTAATAAGTAAAGTTTCTTTTATGACAAATAAGTCCAGAGGAGGCTCTCTCAAC 867
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

705 TGCAGGTAACACACAGCTGTTTGTAGCAAAATGCTGTTTCCGGTTCATCT----- 756
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

868 AACGGGGATATGTCAGAGGTGCTATCTGTGCTTATAAACTAGTACAGATCTAAGGT 927
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

757 -----GATGTTCCGGTGGAGCTATCCATTGTAGCAAAACAGGTTTCAGCACCGACCT 809
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

928 CACCTCTACTGGAATCAGATGTTACTTCTCAGCAACAATACATCGACACAGCGGAGG 987
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

810 TACTATAAGAGATAACAAGTCTTGATTTTGGAGAAATACTTCTTCAGCAAAAGGTGG 869
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

988 AGCTATCTATGTGAAAAAGCTCGAAGTCTGCTTCCGGAGGACTTACCCTATTTCAGTAGAAA 1047
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

870 AGCGATTTACCCGATAAATCATATTGACTTCTGTTGGGCTACGGCAATTATCAATA 929
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

1048 TAGTGTCAATGGAGTACAGCTCTTAAGGTGGAGCCATAGCTATCGAAGTAGTGGGA 1107
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

930 CAAAGTTTACCCATGCTACA---CCTAAGGGTGGAGCTATTGTTATGCTGCCATGGAGA 986
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

1108 ATTGAGTTTATCCGCGGATAGTGGGACATTTGCTTTTATGGGAA---TACAGTCACTTC 1164
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

987 ATGTAGCTTAAACGCTGACATGGGATATTACTTTTGTATTAATTAACCTGTGGCCACA 1046
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

1165 TACTACTCTCTGGGACGAATAGAGTAGTATCGACTTAGGACAGAGTGCAAGATGACAGC 1224
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

1047 AGACAATGCTACAATAAAGAAATGCCAATTAACATTGAAGGCAATGGTAAATTCGTCAA 1106
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

1225 TTTGCGTCTGCTGCTGGTAGGCCATCTATTCTATGATCCCATTAACAGGATCATC 1284
 Db TTTTGTTCAGACTGCAGACCAACCTTTCACAGGTAACGGGAATCTCTATTGTCCA 290

Db CTTAGCTGCAGCGCTCGAAGACGATTTCTTCTATGATCCTTACAGTTG----- 1159

Qy CACAACAGTTACAGATGCTTAAAGTTAATGAGACTCCCGGAGATTCTGCACATCAATA 1344

Db -----AAGGTAATGCTGCTGATCTTCTCACTTTGAATAAAGCTGAGGGTGATAAAGCTA 1214

Qy TACAGGGAACATCATCTTTCACAGGAGAAAAGTTATCAGACACAGAGCGCCAGATTCTAA 1404

Db TAATGGAAGATTATTTTTCAGAGAGAAAGCTCACTGAAGAACAGCTGCTGTGGGA 1274

Qy AAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTTCAGAGGAGTACTCTATCTTAAA 1464

Db TAACTTAAGACAACATTTTACACAGCCTATCACTTTAGCTGCTGGTGAATCTGTGTACG 1334

Qy ACATGGAGTACTCTGAGACTCAGGCACTTCACTCAACAGCAGATTTCTGCTCGAAAT 1524

Db CAGCGGTGGAAGTAGAAGCAAAAACAGTCTGTCGCAACAGCAGGATCTTTGATCTGAT 1394

Qy GAGCTAGGAATCTCTA---GAACCTGCTGATPACTAGCACCATAAACAATTTGCTCAT 1581

Db GGATGAGGCAAAAAGTTATCCGCAAAAACAGAAAGATGCTACACTGACGAATCTGGCTAT 1454

Qy TAAACATCAGTTTCTATAGACGCTGCAAGAGGCAAAATAGAACCAACCAAGCTACGTCAA 1641

Db TATCCGGAATACCTTAGATGGGAAAATTCGCCGTAGTCGATGCCCTTCTGCTGGGAA 1514

Qy AAATCTGACTTTATCTGGAACCATCACTTTATTGGACCCGACGGGACGTTTATGAAA 1701

Db GAATGACTTTATCAGGTGCTATTGGGTTATTGATCTTACAGGGAAGTTTATGAAA 1574

Qy TCATAGTTTAAAGATCTCAGTCTCAGTACATCTTAGAGCTCAAAGCTTCTGGAAGTCT 1761

Db CCATAAGCTTAAATGATACGTTAGCTTTTAGAGGAATTCAACTTCTGGAAGAGTTCCGT 1634

Qy AACAGCAACCCAGTACTCCAGATCTTAAATGGGTGAGAAATTCATTAAGGCTATCA 1821

Db GACAAACCAACCGTCTAGTCTGTTGTTGGTGTGTTGTAACCCACTATGTTATCA 1694

Qy GGGAA-----TTGGGCCCAATTTGTTGGGGACAGGGGCTCTAGGACTGC 1869

Db AGGAACCTGGTCTGCTAGTTGGGTCAAAGATAAATCTGATCTTAAACACAAACAGC 1754

Qy AACCTTCACTGGACTAAATCTGCTATTTCTTAATCCCGAGGCTATCGGCTCTTTAGT 1929

Db AATCTTACCTGGATAAAACAGGATATGTTCCAAATCTCTGAAGCTGCTCGCTAGT 1814

Qy CCTTAATAGCTTATGGAATGATTTATAGATPATTAGCTCTCTCCATTTCTTATGAGAC 1989

Db ACTCAATAGCTTTGGGGATCTTTTATAGATTTACGTTCTATTCAAGATGTTCTTGGAAACG 1874

Qy TGCAAAACGAAGGTTGC---AGGAGACCGTGTCTTTTGGTGTCTGCTGATTTCTAATCT 2046

Db TAGTGTGATAGTATCTTGGAGACAGCTGCTGGTGTGGTCTCTCGAATGCGAACTT 1934

Qy CTTTCATAGGATAGTACAAAACACAGCGGGTTTGGCCATTTGAGTGGCGGTTATGT 2106

Db CTTCCATAAAGATCGAATGCTGAAAATTCGCAATTCGTCATATCAGTTCCGGATATGT 1994

Qy CATAGGAGAACCTTACTTCTGATAGATTTCTTGTAGTGTGCTGCTGATTTGTCAGCT 2166

Db GTTAGAGCCCAACAATAATCTCGAGAGGATTTCTTAGTGTGGCTTTCTGTCAGTT 2054

Qy CTTTGGAAAGATAGAGACTACTTTGTAGCTTAAGATAAGGTAAGTCTACGAGGAAC 2226

Db ATTTGCAAAAGATAAGACTACTTCTTGAAGCAAGAACGCGCAAAACGCTCTATCGGGTTC 2114

Qy TCTCTATTACAGCA-----CAAGAAACCTATATCTCTCTCTCTGCAAACTACGGCC 2280

Db TGTATATTACAGCAATGAGCAAGTTGATGATCTCTACGCGGTTATTAAATGCGGCTAA 2174

Qy TTGTTGCTGTTGCTTATGTTTCTACAGAGATTCCTGTTCTCTTTTTCAGGAAACCTTACGTA 2340

Db 2175 CACGCTGTTTTCAGGGTTTCTAAGAGATTCCTATTTCTTGGATGCACAAATTACCTA 2234
 QY 2341 CACCATAGCGATACGATCTGAAACCAAGATATACAACTATCTACTGTTTAAAGGAAG 2400
 Db 2235 TTGCCACACGGCCAAACATGACAACTGCAACGCTCTATACAGACTATCTGAAAGTGAAGTTC 2294
 QY 2401 CTGGGGGAATAGATGTTTCGGCTTTAGAAATTCGGTGAAGACTCCGATTTGCTTAGATGA 2460
 Db 2295 TTGGGGTAATGATACCTTGGGCTTAACTTTGCTACTAGCTACTATCCGGTATTAG 2354
 QY 2461 AAGTGCTCTATTGAGCAGTACATGCCCTTCATGAAATGAGTTGCTATGACATCA 2520
 Db 2355 TTCTTCTATCTTGTAGTATGCAACCTTTGCAAAATTACAAGTTGCTATGCGCACCA 2414
 QY 2521 GGAAGGTTTAAAGAACACAGGGAACAGAGCTCGTGAATTTGMAAGTAGCCGCTTTGTGAA 2580
 Db 2415 AGATGACTTTAAAGAACCAACACAGAAAGCGGGTCTTTGAAGCAGCGAICTTCTCA 2474
 QY 2581 TCTTGCTTACCTATCGGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACGTA 2640
 Db 2475 CGTTTCTGTACCTATAGGTATATAAAATTTGAGAAACTCTCTATGGAGAGAGTGTCTTA 2534
 QY 2641 CAATCTAATCTTGTGTTACTGATGATCTTGTGATAGTAACCCGACTGTACGACAC 2700
 Db 2535 TGATCTTACATGATATACCTGATGATGATGATGATGATGATGATGATGATGATGATG 2594
 QY 2701 ACTGGAATAGCGGTGATCTTTGGAACACCTTCGGTACGAATTTGGCAAGCAAGCTTT 2760
 Db 2595 ATTGGGATCAATGACGTTTCTCGGTTAACACAGCTACGAATCTTGTAGCAAGCTTT 2654
 QY 2761 AGTCTTCTGTCAGGGAACCAATTTGCTTTTAACTCAAAATTTGAGCCTTTAGCCAA 2820
 Db 2655 CATAGTTCGCGGGTAAACATATTCGCTTAACTTACCTTCTGCTGTGATGATGTTCA 2714
 QY 2821 TTCTTTTGAATTCGCGGTGATCTCGCAATTTACAAATGATAGACTGAGGACAAATACCA 2880
 Db 2715 TGGTTTGAATTTACGAAGCTCTTCAAGAAATATACGATAGTCTTGGCGCTAAGTTCG 2774
 QY 2881 ATTCTAA 2887
 Db 2775 GTTCTAA 2781

RESULT 6

ABQ78033
 ID ABQ78033 standard; DNA; 2781 BP.

XX AC ABQ78033;

XX DT 03-OCT-2002 (first entry)

XX DE Chlamydia polynucleotide SEQ ID NO 56.

XX KW Chlamydia; antibacterial; vaccine; immune response; infection; gene; ds.

XX OS Chlamydia psittaci.

XX PN WO200247718-A2.

XX PD 20-JUN-2002.

XX PF 17-DEC-2001; 2001WO-US48773.

XX PR 15-DEC-2000; 2000US-255839P.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Johnston SA;

XX DR WPI; 2002-583472/62.

XX DR P-PSDB; ABB98228.

XX PT Vaccine useful for immunizing an animal, comprising at least one

PT polynucleotide having a Chlamydia sequence or at least one Chlamydia
 antigen
 PS Claim 6; Page 167-168; 183pp; English.
 XX The invention relates to a vaccine (I) comprising at least one
 polynucleotide (ABQ78033-ABQ78039) having a Chlamydia sequence or at
 least one Chlamydia antigen (ABB98203-ABB98234) and a pharmaceutically
 acceptable carrier. The antigens are useful for immunising an animal, by
 providing at least one Chlamydia antigen or its antigenic fragment to the
 animal, in an amount effective to induce an immune response in the animal
 e.g. mammals including bovine or human. The method is effective to induce
 an immune response against C. psittaci, C. pneumoniae or non-Chlamydia
 infection. The method further involves administering to the animal an
 antigen or an antigenic fragment from Chlamydia species other than
 C. psittaci or C. pneumoniae or an antigenic fragment from a
 non-Chlamydia species.

XX SQ Sequence 2781 BP; 818 A; 555 C; 610 G; 798 T; 0 other;

Query Match 18.2%; Score 546.6; DB 24; Length 2781;

Best Local Similarity 53.7%; Pred. No. 4.2e-141;

Matches 1390; Conservative 0; Mismatches 1134; Indels 63; Gaps 10;

QY 328 TTTTAAACACACTAAGGGGATTTGACCTTTACAGGTAAACGGAACTCTTATTGTTCCA 387
 Db 231 TTTTGTTCAGACTGCAGACAACTTAACCTTCAAGGGAAACCAACCATAGCTTTATCCATAAC 290
 QY 388 AACGGTGGATGACAGGACTGTAGCAGGGGCTGCTTTAACAGCAGCGTGGTAGATAAATC 447
 Db 291 GAACCGAATGCGGAGCTAATCC---TGCGGAATTAACGTTAACACTGCCGATAGAT 347
 QY 448 TACACGTTTATAGGGTTTTCCTGCTATCTTTTATATTCGGTCTCCTGGAAGTTCGATAAC 507
 Db 348 TCTTACGCTGACAGATTTTCTTAAGTTAGCTTTAAGGAATGCCCATCTTCTCTAGTGA 407
 QY 508 TACCGCAAGAGCGGCTGTAGCTGTACGGGTAGCTTTGAGTTTGCACAAAATATGTCAG 567
 Db 408 TACTGSAAGAGGGC---TATGAATTCGGAGGACATTAACCTTAGCGAATATGCGAG 464
 QY 568 TTGCTCTTTCAGCAAAAATTTTCAACCGATAATGCGGCTGTATCACCGCAAAAATCT 627
 Db 465 TATTCTGTTTGTATCAGAACTATTCGCTGAGAATGGTGAGCCATCTCTTGCAAAAGCTTT 524
 QY 628 TTTATTAACAGGACTACAAATGCTAGCTCTGTTTCTGAATATACCTCTCAAGAGAG 687
 Db 525 TTCTCTAACCGGCTGAGCAAGAAATCAGCTTCAACCTACTCTACTGCGAAAAAAGG 584
 QY 688 CGGAGCATTTCAGACTTCCGATGCCCTTACCAATTACTGGAACCAAGGGGAGTCTCTTT 747
 Db 585 TGGAGCGATTGCTGTCTACGGGAATAGCTCATCTTTTCGGACACCAAGGCACAACTCAGATT 644
 QY 748 TTCTGACATATCTTCTCGGATCTGGAGCTGCAATTTTACAGAGCTCGGTGACTAT 807
 Db 645 TTCTGGAACACTGCTGTGAATTTCTGGGGGAGCAGTATATTACAGAACTCTTATGACCAT 704
 QY 808 TTCTAATAATGCTTAAAGTTTCTCTTATTGACAAATAAGGTCACAGAGCGAGCTCTCTCAAC 867
 Db 705 TGCAGGTACACACCGTTGCTTTTAGCAACAACTGCTGTTTCGGTTTCATCT- 756
 QY 868 AACGGGGATATGTCAGAGGCTGCTATCTGCTTATATAAACTAGTACAGATACATAAGGT 927
 Db 757 -----GATGGTTGCGGTGGAGCTATCCATTTGTAGCAAAAACAGGTTTCAGACCGACCT 809
 QY 928 CACCTCACTGGAATCAGATGTTACTCTTTCAGCAACATATCATCGAACAGCGGGAGG 987
 Db 810 TACTATAAGAGATAACAAAGTCTTGATTTTGGAGGAATACTTCTTTCAGCAAAAGGTGG 869
 QY 988 AGCTATCTATGTGAAAAAGCTCGAACTGGCTTTCCGAGGACTTACCTCTTTCAGTAGAAA 1047
 Db 870 AGCGATTACACCGATAAAGTCTTATTTGACTTCTGTTGGCCCTACGGCATTTATCAATAA 929
 QY 1048 TAGTGTCAATGGAGGTACAGCTCTTAAAGGTGAGCCATAGCTATCGAAGATAGTGGGA 1107

Db 930 CAAAGTTACCCATGCTACA---CCTAAGGGTGGAGCTATTGGTATTTGTCGCAATGGAGA 986
 Qy 1108 ATTGAGTTATTCGCCGATAGTGGTGACATTTGCTTTTGGGAA---TACAGTCACTTC 1164
 Db 987 ATGTAGCTTTAACCGTGAACATGGGATATTACTTTTGTATTAATTAACCTGTATGGCCACACA 1046
 Qy 1165 TACTACTCCTGGGACGAATAGAAAGTATGATCGACTTAGAAACGAGTGCACAAAGATGACAGC 1224
 Db 1047 AGACAATGCTACAATAAAGAAAGAAATGCCAATTAAACATTGAAGGCAATGGTAAATTCGTCAA 1106
 Qy 1225 TTGCGTCTGCTGCTGTAGAGCCATCTACTCTATGATCCCATTAATACTACAGGATCATC 1284
 Db 1107 CTTAGCGTGGGCTGTGAAGACGATTTCTTTCTATGATCCTATCACAGTTG----- 1159
 Qy 1285 CACAAAGTTACAGATGCTTTAAAGTTAATAGAGCTCCGCGAGATTTCTGCACATAA 1344
 Db 1160 -----AAGGTATGCTGTGATCTTCTCACTTGAATAAAGCTGAGGGTGATAAAACGTA 1214
 Qy 1345 TACAGGACATCATCTTCAAGGAGAAAGTTATCAGACAGAGCGCCGACAGATTTCTAA 1404
 Db 1215 TAATGGAAGAAATATTTTTCAGGAGAAAGCTCACTGAAGAACAAAGCTGCTGTGGCGA 1274
 Qy 1405 AATCTCTACTTCCGAAGTACTACAGCCTGTAACTCTTTACAGAGGTACTCTATCTTTAAA 1464
 Db 1275 TAACTTAAGRCAACATTTACACAGCCCTATCATTAGTCTGTGAACTTTGTTAGC 1334
 Qy 1465 ACATGGAGTGACTTCAGAGCTCAGGCAATCACTCAACAGGAGATTCCTGCTCGAAAT 1524
 Db 1335 CAGCGGTGTGAAGTAGAAGCAAAACAGTGTGCAAAACAGCAGGATCTTTGATTCTGAT 1394
 Qy 1525 GGAGCTAGGAACTACTCTA---GAACTGCTGATAGTACAGCCATAAACAATTTGGTCA 1581
 Db 1395 GGATCGAGCAAAAGTTATCCGCAAAACAGAGATGCTACAGCGAATCTGGCTAT 1454
 Qy 1582 TAACATCAGTTCTATAGACGTCGAAAGAGGCAAAATAAGAAACCAAAGCTACGTCAAA 1641
 Db 1455 TAATCCGAATACCTTAGATGGGAAATAATTCGCCGTAGTCGATGCCGTGTGCTGGGA 1514
 Qy 1642 AATCTGACTTTATCTGGAACCATCACTTTATGACCCGAGCGGACGTTTATGAAA 1701
 Db 1515 GAATGTACTTTATCAGGTGCTATTGGCGTTATTGATCCTACAGGGAAGTTTATGAAA 1574
 Qy 1702 TCATAGTTTAAGAAATCTCAGTCTCAGACATCTTAGAGTCAAAAGCTTCGGAACGT 1761
 Db 1575 CATAAGCTTAATGATACGTTAGCTTTAGGAGGAATTCACCTTCTGGGAAGGTTCCGT 1634
 Qy 1762 AACAGACCGCAGTGAATCCAGATCCTAATATGGGTGAGAAATTCCAATTACGCTATCA 1821
 Db 1635 GACAAACAAACCAACGTCCTAGTCACTGTTGTTGGTGTGCTGAAACCCCACTATGTTATCA 1694
 Qy 1822 GGGAAC-----TTGGGGCCCAATGTTTGGGGACAGGGGCTTCTACGACTGC 1869
 Db 1695 AGAAACTGGTCTGTGCTAGTTGGGTCAAGATTAATTAACCTGATCTCAAAACACAAACAGC 1754
 Qy 1870 AACCTTCAACTGGACTAAAACCTGCTATATTCCTAATCCGAGGCTATCGGCTCTTTAGT 1929
 Db 1755 AATCTTTACCTGGAATAAAGAGGATATGTTCCAAATCCTGAAACGTCGTGCTCCGCTAGT 1814
 Qy 1930 CCTAATAGCTTATGGAATGCAATTTATAGATTTAGTCTCTCCATTTATCTTTATGGAGAC 1989
 Db 1815 ACTCAATAGCCTTTGGGATCCCTTTATAGATTTAGCTTTCTATTCAAGATGCTTTGGACG 1874
 Qy 1990 TGCAAACGAAGGTTGTC---AGGAGACCGTCTCTTTTGGTGTGCTGGATTAATCTAACTT 2046
 Db 1875 TAGTGTGTATGATATCTTGACACAGCTGCTGGTTTGGGTCTCTGGAATGGGAACCTT 1934
 Qy 2047 CTTCCATAGGATAGTACAAAACAGCAGCGGGGTTTCGCCATTTAGTGGCGGTTATGT 2106
 Db 1935 CTTCCATAAAGATCGGAATGCTGAAATCGCAAAATTCGTCATATCAGTTCGGGATATGT 1994
 Qy 2107 CATAGGAGAACCTACATACCTTTGTCATAGATTTCTAGTGTGCTGCAATTTGTCAGCT 2166

Db 1995 GTTAGGAGCACAACAATAACCTCGAGAGAGGATTTCTCTAGTGGCTTTCTGTCACTT 2054
 Qy 2167 CTTTGGAGAGATAGAGACTACTTTGTAGCTAAGATCAAGGTACAGTCTACGGAGGAAC 2226
 Db 2055 ATTTGCAAAAGATTAAGACTACTTTGTAAAGCAAGAACGCCGCAACGCTATCGGGTTC 2114
 Qy 2227 TCTCTAATTAACAGCA-----CAACGAAACCTATATCTCTTTCTGCAACATACAGGCC 2280
 Db 2115 TGTATATTATCATGCATGTGAGCAAGTTTGTATGATCTCAGCGGTTTATTTAATGGGCTAA 2174
 Qy 2281 TTGTTGTTGTTCTTATGTTTCTACAGAGATTCCTGTTCTCTTTTTCAGGAAACCTTAGCTA 2340
 Db 2175 CAGCTGTTGTCAGGGTTTCTAAGAGATTCCTATTTTCTTGGATGCAAAATTACCTA 2234
 Qy 2341 CACCCATACGGATAACGATCTGAAACCAAGTATACAAATATCTCTACTGTTTAAAGGAAG 2400
 Db 2235 TTGCCACACGCGCAACACATGACCAACGCTCTATACAGACTATCTGAAAGTGAAGGTTTC 2294
 Qy 2401 CTGGGGGATGATAGTTTTCGCTTTAGAAATTCGGTGAAGAGCTCCGATTTGCTTAGATGA 2460
 Db 2295 TTGGGTAATGATACCTGGGCTTAACTTTGTCTACTAGCGTACCTATCCCGGTATTTAG 2354
 Qy 2461 AAGTGTCTTATTTGAGCAGTACATGCCCTTTCATGAAATTCAGATTTGCTATGCACATCA 2520
 Db 2355 TTCTTCTATCTTTGATAGTTATGCAACCGTTTGCAGAAATTTACAGTTTGTCTATGCGACCA 2414
 Qy 2521 GHAAGTTTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGTACGCGTCTTTGTGAA 2580
 Db 2415 AGATGACTTTTAAAGAACCAACCAACAGAGAGCGCGGCTCTTTGAAAGCAGCGATCTTCTCAA 2474
 Qy 2581 TCTTGTCTTACCTATCTCGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACGTA 2640
 Db 2475 CGTTTCTGTACCTATAGGTATAAATTTGAGAACTCTCTATGAGAGAGAGTGTCTTA 2534
 Qy 2641 CAATCAACTCTTGGTTATCTGTGATCTTGTTCGTAGTAACCCCGACTGTPACGACAAAC 2700
 Db 2535 TGTATCTTACACTGATGATATATACCTGATGTGACCGTCATAATCCAAGCTGTATGACAGG 2594
 Qy 2701 ACTGCGAATTTAGCGGTGATTTCTTGAAGAACCTTCGTTACGATTTGGCAAGCAGACTTT 2760
 Db 2595 ATTGGGATCAATGACGTTCTCTGTTAACCAACAGCTACGAATCTTGTAGCAAGCTTT 2654
 Qy 2761 AGTCCTTCGTGAGGGAACCATTTTGTCTTAACTCAAAATTTGAAGCCTTTAGGCCAAT 2820
 Db 2655 CATAGTTTCGCGGGTAACCATATTGCCCTTAACCTCTGCTGTTGAGATCTTCAGTCAGTT 2714
 Qy 2821 TTTCTTTGAATTCGTTGGTCTATTCGCAATTAACATGTAGACTTTAGGAGCAAAATACCA 2880
 Db 2715 TGGTTTCAATTAACGAAGCTCTTCAAGAAATTTATAACGTAGATCTTGGCGCTAAGGTGCG 2774
 Qy 2881 ATTCTAA 2887
 Db 2775 GTTCTAA 2781

RESULT 7
 ABX99200

ID ABX99200 standard; DNA; 2781 BP.

XX AC ABX99200;

XX XX 20-MAY-2003 (first entry)

XX C. psittaci genomic DNA sequence CP4 #12 #2.

XX DNA vaccine; chlamydia infection; blindness; mastitis; infertility;
 XX abortion; sexually transmitted disease; atherosclerotic plaque; ds;
 XX community-acquired pneumonia; coronary heart disease.

XX Chlamydia psittaci.

XX US2002183272-A1.

XX

PD 05-DEC-2002.
 XX 17-DEC-2001; 2001US-0023437.
 XX 16-AUG-2000; 2000US-225839P.
 XX (JOHN/) JOHNSTON S A.
 PA (STEM/) STEMKE-HALE K.
 PA (SYKE/) SYKES K F.
 PA (KALT/) KALTENBOECK B.
 XX Johnston SA, Stemke-Hale K, Sykes KF, Kaltenboeck B;
 XX WPI; 2003-328634/31.
 DR P-PSDB; AB066284.
 XX
 XX New vaccine comprising a polynucleotide with a Chlamydia sequence or a
 PT Chlamydia antigen, for inducing an immune response against Chlamydia
 PT psittacci, Chlamydia pneumoniae, other Chlamydia species, or a
 PT non-chlamydia infection -
 XX
 PS Claim 6; Page 74-76; 100pp; English.
 XX
 CC The invention relates to a vaccine comprising a pharmaceutical carrier
 CC and at least one polynucleotide having a Chlamydia sequence or at least
 CC one Chlamydia antigen. The polynucleotide sequences are obtained
 CC from cloned expression library of fragmented genomic DNA (expressed in
 CC the vector pCMV-Ubi(+P3)). Also included are immunising an animal
 CC comprising providing to the animal at least one Chlamydia antigen or its
 CC antigenic fragment (expressed from the cloned polynucleotides) to induce
 CC an immune response (the proteins are chosen by transforming a vertebrate
 CC animal with constituents of the library and choosing those which elicit
 CC the best immune response, and then expressing those clones in cell
 CC culture and purifying the protein), preparing antibodies against a
 CC Chlamydia antigen (comprising identifying a Chlamydia antigen that
 CC confers immune resistance against chlamydia bacterial infection when
 CC challenged with the Chlamydia species in which the antigen was prepared,
 CC generating an immune response in a vertebrate animal with the identified
 CC antigen, and obtaining antibodies produced in the animal, the antibodies
 CC are used to assay for the presence of chlamydia infection in a vertebrate
 CC animal) and testing for antigens for a first disease state/infectious
 CC agent (comprising determining an antigenic polypeptide or a nucleic acid
 CC encoding an antigenic polypeptide from a second disease state or
 CC infectious agent, obtaining a homologue of the antigenic polypeptide or
 CC a nucleic acid encoding an antigenic polypeptide from a second disease
 CC state or infectious agent for the first disease state/infectious
 CC agent, and testing the homology to see if it is an antigenic
 CC polypeptide or a nucleic acid encoding an antigenic polypeptide for the
 CC first disease state or infectious agent). The vaccine, antigens and
 CC polynucleotides are useful for inducing a protective immune response in
 CC vertebrate animals against *C. psittacci*, *C. pneumoniae*, other species of
 CC Chlamydia, or a non-chlamydia infection. The antigens are also useful for
 CC antibody preparation techniques. Chlamydia species are responsible
 CC for blindness, sexually transmitted disease, community-acquired
 CC pneumonia and act as co-factors in atherosclerotic plaque formation in
 CC coronary heart disease. *C. psittaci* in particular is a cause of mastitis,
 CC infertility and abortion in cattle. The present sequence is one of the
 CC cloned Chlamydia psittaci genomic DNA fragments of the invention.
 XX
 SQ Sequence 2781 BP; 818 A; 555 C; 610 G; 798 T; 0 other;
 Query Match 18.2%; Score 546.6; DB 25; Length 2781;
 Best Local Similarity 53.7%; Pred. No. 4.2e-141;
 Matches 1390; Conservative 0; Mismatches 1134; Indels 63; Gaps 10;
 328 TTTTAAACACACTAAGGGCGATTGACTTTTCACAGGTACGGGAATCTCTATTGTGTCCA 387
 231 TTTTGTTCAGCTGCAGACAACTTAATTTTCAAGGGAACACCATAGCTTAATCATAC 290
 388 AACGGTGTAGGAGCTGTAGCGGGCTCTGTATTAACAGCAGCGTGTAGATAAATC 447
 291 GAACGCGAATGCCGAGCTAATCC---TCCGGGAATTAACGTTAACACATGCCGATAAGAT 347

QY 448 TACCACGTTTATAGGGTTTCTTCGCTATCTTTTATTTGCGTCTCTCTGGAAGTTTCGATAAC 507
 DB 348 TCTTACGCTGCACAGATTTTCTTAAGTTTGAAGTTTAAAGTATCCCATCTTCTCTAGTGAA 407
 QY 508 TACCGGCAAGAGGCGGTGTAGCTGCTCTACGGGTAGCTTTGAGTTTGACAAAAATGTCTAG 567
 DB 408 TACTGGAAAAGGGGC---TATGAAATCCGGAGGAGCATTAATCTTAGCGAATAATGCCAG 464
 QY 568 TTTTGTCTTTCAGCAAAAACCTTTTCAACGGATTAATGCGGTGCTATCACCGCAAAACCTCT 627
 DB 465 TATTCTGTTTGTATCAGACTATTTCGCTGAGAAATGTTGGAGCCATCTCTTTCAGAAAGCTTT 524
 QY 628 TTCTTAAACAGGGACTTACAAATGTCTAGCTCTGTGTTTCTGAAAAATACCTCTCTCAAGAAAGG 687
 DB 525 TTCTCTAACCGGCTCGAGCAAAAGAAATCAGCTTCCACCACTAATCTCTACTGCGAAAAAGG 584
 QY 688 CGAGGCCATTACAGCTTCGATCGCCCTTACCAATTAAGTGAACCAAGGGAAGTCTCTTT 747
 DB 585 TGGAGCGATTGCTGCTACGGGAATAGCTCATCTTTTCGGACCAACCAAGGCACAAATCAGATT 644
 QY 748 TTCTGACAAATCTCTTTCGGATTCTGGAGCTGCAATTTTACAGAAAGCTCGTGACTAT 807
 DB 645 TTCTGGGAACCTGCTGTGAATTTCTGGGGAGCAGTATATTTCGAAAGCTTCTATGACGAT 704
 QY 808 TTCTTAATATGTAAAGTTTCCCTTTATTGACAAATAGGTACAGGAGGAGCTCTCTCAAC 867
 DB 705 TGCAGGTAAACACACGTTGCTTTTAGCAACAATGCTGTTTCCGGTTCATCT- 756
 QY 868 AACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTTATAAACTAGTACAGATCTAAGGT 927
 DB 757 -----GATGTTCCGGTGGAGCTATCCATTTGTAGCAAAACAGGTTTTCAGCACCCACCT 809
 QY 928 CACCTCTCATCTGAAATCAGATGTTTACTCTTTCAGCAACAATATACATCAGCAACAGCGGGAGG 987
 DB 810 TACTATAAGAGATAACAAGTCTTCAATTTTTCAGGAAATACTTCTTTCAGCAAAAGGTGG 869
 QY 988 AGCTATCTATGTGAAAAAGCTCGAACTGGCTTCCGGAGACATACCCCTATTTCAGTAGAAA 1047
 DB 870 AGCGATTTTACACCGGATAAATCATATTGACTTCTGTTGGGCTACGGCATTTATCAATAA 929
 QY 1048 TAGTCTCAATGAGGTACAGCTCTCTTAAGGTGGAGCCATAGTATCGAAGTAGTGGGGA 1107
 DB 930 CAAAGTTTACCCTGCTACA---CCTAAGGGTGGAGCTATTGGTATTTGTCCTCAATGAGGA 986
 QY 1108 ATTGAGTTTATCCGCCGATAGTGTGACATTTGCTTTTATAGGGA---TACAGTCACTTC 1164
 DB 987 ATGTAGCTTAAACCGCTGAACATGGGATATTACTTTTGTATTAATACCTGTATGGCCACACA 1046
 QY 1165 TACTACTCTGGGAGCAATAGAGTAGTATCGACTTTAGGAACAGAGTGAAGATGACAGC 1224
 DB 1047 AGACAATGCTACAATAAAAGAAATGCCAATTAACATTTGAAGCAATGTTAAATTCGTCAA 1106
 QY 1225 TTTTGGTTTCTGCTGCTGTAGAGCCATCTCTCTATGATCCCATCTACAGGATCATC 1284
 DB 1107 CTTAGTGCAGGGTCTGAAAGACGATTTCTTTTATGATCTCTATCAGATG----- 1159
 QY 1285 CACAACTTACAGATGCTTTAAAGTTTAATGAGACTCCGGCAGATTTTCGACTACAATA 1344
 DB 1160 -----AAGGTAATGCTGCTGATCTTCTCACTTTGAATAAAGCTGAGGTGATAAACCTGA 1214
 QY 1345 TACAGGGAACATCATCTTTCAGGAGAAAAAGTTTATCAGAGACAGAGCCGAGATTTCAA 1404
 DB 1215 TAATGGAAGAATTTATTTTTCAGGAGAAAAAGCTCACTGAAGAAACAAGTCTGTTTGGGA 1274
 QY 1405 AAATCTTACTTTCGAGCTACTACAGCCCTGTAACTCTTTTTCAGAGGTTACTCTATCTTTAA 1464
 DB 1275 TAACTTAAGAACATTTTACAGCCCTATCACCTTTAGCTCTGTTGAACTTTGTTTACG 1334
 QY 1465 ACATGGAGTGTACTTCGAGACTCAGGCAATTCACCTCAACAGCAGGATTTCTGCTTCGAAAT 1524
 DB 1335 CAGCGGTGTGGAAGTAGNAGCAAAAACAGTGTGCAACAGCAGGATTTTGTATCTGAT 1394
 QY 1525 GGAGTAGGAACCTACTCTA---GAACCTGTGTGATCTAGTACCAACATAAACAATTTGGTCAAT 1581

CC proteins; (6) a purified polypeptide composition comprising at least 50
CC weight % of P1; and (7) a monoclonal antibody binding specifically to the
XX peptide of (6).

SQ Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 other;

Query Match 17.7%; Score 531.2; DB 21; Length 273254;

Best Local Similarity 53.0%; Pred. No. 7.6e-136; Indels 74; Gaps 10;

Matches 1415; Conservative 0; Mismatches 1183;

QY 247 TCGTGGAACTACCTACCTATTTAAGGGAATGCTCACTCTAGAAAATATTCCTGGAAACAGG 306

DB 98349 TACTGGATAGACTATACCTCTGACAGGAGATATACTCTGCAAAACCTTTGGGATTGCG- 98407

QY 307 CACAGCAATCAAAAAGCTGTTTTAAACAACATAAGGCGATTTGACTTTTCACAGGTAA 366

DB 98408 --CAGCTTTAAGCAAGGGTGTGTTTTCTGACACTACGGAATCTTTAANGCTTTGCCGGTAA 98465

QY 367 CGGGAACCTCTATTGTTCCAAAACGGTGGATCGAGGACTGTAGCAGGGCTGCTGTGTTAA 426

DB 98466 GGGGTACTCATTCTCTTTTAAATATTAAGTCTAGTCTGAAGCGCAGCACTTCTGT 98525

QY 427 CAGCAGCGGTGAGATAAATCTACACGTTTATAGGGTTTTCTTCGCTATCTTTTATTGC 486

DB 98526 TACAACTGATAAAAATCTGTGCTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCC 98585

QY 487 GTCCTCTGGAATTCGATAAATACCGGCAAGAGCGCTAGTCTCTACGGGTAGCTT 546

DB 98586 ATCATCGGTATCAACACCCCTCAGGAAAGGTGCACTTAATGTGGAGGGATC---T 98642

QY 547 GAGTTTGACAAAATGTCAGTTGCTCTTCAGCAAAAACCTTTCAACGGATATATGGCG 606

DB 98643 TACATTTGATACAAATGAACTATTTTATTTAACAAGATTTACTGTGAGGAAATATGGCG 98702

QY 607 TGCTATCACCCGAAAACCTCTTTCAATTAACAGGACTACAATGTCAGCTCTGTTTCTGA 666

DB 98703 AGCCATTTCTACCAAGATCTTTCTTTGAAAAACAGCACGGATCGATTTCTTTGAAAG 98762

QY 667 AAATA-----CCTCCTCAAGAAAGGGAGCCATTACAGACTCCGATGCCCTTAC 717

DB 98763 GAATAAATCGAGGCAACAGGGAATAAGGTGGGCTATTTGTGCTACTGTGTACTGTAGA 98822

QY 718 CATTACTGGAACCAAGGGGAAGTCTCTTTTCTGCAATATCTTCTCGGATTTCTGGAGC 777

DB 98823 TATTACAAATAATACGGCTCCTACCTCTCTCGAAATATTTGCTGAAGTCTGAGGTG 98882

QY 778 TGCAATTTTACAGAGCCTCGGTGACTAATTTCTTAATGCTAAAGTTTCTTTTATGA 837

DB 98883 AGCTATAAATAGCACAGGAAACTGTACAAATACAGGGAATACGCTCTCTGTATTTCTGA 98942

QY 838 CAATAAGGTACAGAGCGAGCTCTCAACACGGGGGATATGTCAGGAGGTGCTATCTG 897

DB 98943 AAATAGTGTGAC---AGCGACCGAGGAATGAGGAGCTCTTTCTGGAGATGCG--- 98995

QY 898 TGCTTTAATAAATACTAGTACATAAGGTCAACCTCACTCGAATACAGATGTTACTCTT 957

DB 98996 -----ATGTTACCATATCTGGGATCAGAGTGTAACTTT 99029

QY 958 CAGCAACAATACATCGAACAGCGGAGAGGACTATCTATGTGAAAAGCTCGAACTGGC 1017

DB 99030 CTCAGGAAACCAAGCTGTAGCTAATGGCGAGCCATTTATGCTAAGAAGCTTACACTGGC 99089

QY 1018 TTCGGGAGGACT-----TACCTATTTCAGTAGAATAGTCTCAATGAGGTACAGTCCCT 1072

DB 99090 TTCGGGGGGGGGGGTATCTCTCTTTCTTAACAATATAGTCTCAAGGTACCACTGCAGGT 99149

QY 1073 AAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAAATTTGATTTTATCCCGCATAGTGGT 1132

DB 99150 AATGTTGAGCCATTCTATCTGCGAGCTGGAGAGTGTAGTCTTTTCAGCAGAAAGCAGGG 99209

QY 1133 GACATTCCTTTTTCAGGAATACAGTCACTTCTACTACTCC---TGGGACGAATAGAAGT 1189

DB 99210 GACATTAACCTTCAATGGGAATGCCATTTGTTGCAACTACACCACAACTACAAAAGNAAT 99269

QY 1190 AGTATGAGCTTAGGAAGCAGATGCAAAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGACC 1249

DB 99270 TCTATTGACATAGGATCTACTGCAAGATACAGAAATTTACGTGCAATATCTGGGCATAGC 99329

QY 1250 ATCTACTTCTATGATCCCATAACTACAGGATCATCCAAACAGTTACAGATGCTTTAAAA 1309

DB 99330 ATCTTTTCTACGATCCGATTTACTGCTTAATACGGCTGCGGATTTCTACAGATACTTTAAAT 99389

QY 1310 GTTAATGAGACTCCGGCAGATTTGCACTACAAATATACAGGGAACATCATCTTCACAGGA 1369

DB 99390 CTCATAAGGCTGATGAGGTAAATAGTACAGATTAATAGTGGTGCATTTGTTTTCTGGT 99449

QY 1370 GAAAAGTTATCAGAGACAGAGCGCGAGATTTCTAAAAATCTTACTTCGAAGCTACTACAG 1429

DB 99450 GAAAAGCTCTCTGAAGATGAAGCAAAAAGTTGCAGACAACTCACTTCTACGCTGAAGCAG 99509

QY 1430 CCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAAATGAGAGTACTCTGACAGCTCAG 1489

DB 99510 CCTGTAACTCTAACTGAGGAAATTTAGTACTTTAAACGTGGTGTCACTCTCGATACGAAA 99569

QY 1490 GCATTCACCTCAACAGGAGATTTCTGCTCTGAAATGACGTAGGAATCTACTCTAGAACC- 1548

DB 99570 GGCCTTACTCAGACCGCGGTTCTCTGTTATTAATGATCGGSCACAACGTTAAAAAGCA 99629

QY 1549 --TCTGATACTAGCACCATTAACAATTTGGTCAATTAACATCAGTTCTATAGACGGTGA 1606

DB 99630 AGTACAGAGAGGTCACTTTAAACAGGTCTTTCCATTCCTCTAGACTCTTTAGGCGAGGT 99689

QY 1607 AAGAAGCAAAAATAGAAAACCAAGCTACGTCAAAATCTGACTTTTATCTGNAACCATC 1666

DB 99690 AAGAAAGTTGTAATTTGCTGCTTCTGACAGCAAGTAAATAATGAGCCCTTAGTGGTCCGATT 99749

QY 1667 ACTTTATGGACCGGACCGGACGCTTTTATGAAAATCATAGTTTAAAGAAATCTCTCAGTCC 1726

DB 99750 CTTCTTTTGATTAACCAAGGGAATGCTTTATGAAAATCACGACTTAGGAAAACCTCAAGAC 99809

QY 1727 TAGACATCTTAGAGCTCAAGCTCTTGGAACTGTGTAAACAGACCCGAGTGACTTCCAGAT 1786

DB 99810 TTTTCATTTGTGACGCTCTCTGCTCTGGTACTGCAACAACTACAGATGTTCCAGCGGT 99869

QY 1787 CCTATAATGGTGAAGAAATTCCTATACGCTATCAGGGAATCTGGGCCCAATTTGTTGG 1846

DB 99870 CCTACAGTGAACCTCTACGCAATATGGTATCAAGGTACTTGGGGAATGACTTGGGTT 99929

QY 1847 G-----GGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTGAATAAACTGGC 1894

DB 99930 GATGATACCCGAAGCACTCCAAAGACTTAAGACAGCGACATTTAGCTTGGACCAATACAGGC 99989

QY 1895 TATATTCCTTAATCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTT 1954

DB 99990 TACCTTCGGAATCCTGAGCGTCAAGGACCTTTAGTTCTTAATAGCCCTTTGGGATCTTTT 100049

QY 1955 ATAGATATTAGCTCTCTCCATTTATCTTATGAGACTGCAACCAAGGGTTGCAAGGAGAC 2014

DB 100050 TCAGACATCAAGCGAATCAAGGTGCTATAGAGAGTGTCTTTGACTCTTTCTTCTCAGAT 100109

QY 2015 CGTGTCTTTTGTGTGCTGGATTTATCTTCTTCCATAAGGATAGTACAAAAACACCA 2074

DB 100110 CGAGGCTTCTGGGCTCGGGAGTCGCCAATTTCTTAGATAAAGATAAGAAAGGGGAAAAA 100169

QY 2075 CGCGGGTTTCGCCATTTAGTGGCGGTTATGTCAATAGGAGGAAACCTTACATCTTGTCA 2134

DB 100170 CGAAATACCGTCATAAATCTGGTGGATATGCTATCGAGGTGCGAGCAAACTTCTTCT 100229

QY 2135 GATAAGATCTTAGTCTGATTTTCTGAGCTTTTGGAGAGATAGAGACTACTTTGTA 2194

DB 100230 GAAACCTTAATAGCTTTGCTTTTTCCTTTTGGTGGTGGTAAAGATTTCTTAGTC 100289

QY 2195 GCTAAGAAATCAAGGTACAGTCTACGGAGGAATCTCTATTACCAGCACACCAACCTAT 2254

DB 100290 GCTAAGAAATCACTACTGATACCTATGCGAGGCGCTTCTATATCCACACATTAAGAAAT 100349

QY 2255 ATCTCTCTTCCTGCAAACTACGGCTTGTTCGTTCTTATGTTCTCTCAGAGATTCT 2314
 Db 100350 AGTGGGTTCAATAGTGTCTCTTAGATAAA---CTTCTGGCTCTGGAGCTATAACCC 100406
 QY 2315 GTTCTCTTTTTCAGGAACTCTAGCTACACCCATACGGATAACGATCTGAAACCAAGTAT 2374
 Db 100407 CTCGTTTTAGAGGGCAGCTCGCTTATAGCCACGCTCAGTATGATCTGAAGACAGATAT 100466
 QY 2375 ACAACATATCTCTGTTTAAAGGAGCTGGGGAGTATGATGTTTCGTTTAGAATTCGGT 2434
 Db 100467 ACTGGGATCTCTGAGGTGAAAGGTTCTTTGGGGATAATGCTTTTAAACATGATGTTGGGA 100526
 QY 2435 GGAAGAGCTCCGATTTGCTTAGATGAAAGTCTCTATTTCAGCAGTACATGCGCCCTCATG 2494
 Db 100527 GCTTCTCTCATCTTATCTCTGATACCTGCTGATTTGTTGATCTATGCTCCATCATC 100586
 QY 2495 AAATGCGAGTTTGTCTATGCAATCAGGAAGGTTTAAAGACAGGGAACAGAGCTCGT 2554
 Db 100587 AAATGCAATCTGACCTATATACGTCAGGACAGCTTCTCGGAGAAAGGTACAGAGGAAGA 100646
 QY 2555 GAATTTGGAAGTAGCGCTTGTGAACTCTTGCCTTACCTATCGGGATCCGATTTGATAAG 2614
 Db 100647 TCTTTTGATGACAGCAACTCTCTCAATTTATCTTTGCTATAGGGTGAAGTTGAGAAG 100706
 QY 2615 GAATCAGATGCAAGATGCAAGTACAACTCTCTGTTGTTATCTGTTGATCTGTTGTT 2674
 Db 100707 TTCTCTGATTTGAATGACTTTTCTTATGATCTGACTTTTATCTATGTTCTGATCTTATC 100766
 QY 2675 CCFAGTAACCCGCTGTACGACACACTGCGAATTAGCGTGATCTTTCGAAACCTTC 2734
 Db 100767 CCAATGATGCCAAATGCACTACAGCACTTGTATCAGGAGGCTCTTGGGAACTTAT 100826
 QY 2735 GGTACGAATTTGGGAGCAAGCTTTAGTCTCTTGTGCGAGGAACCAATTTTGTCTTAAC 2794
 Db 100827 GCCAATACTTAGCAGCAGGCGCTTGCAGTGCGTGCGAGCAGTCACTACGCTTCTCT 100886
 QY 2795 TCAGATTTGAGCCTTTTAGCAATTTCTTTTGAATTCGTTGGTCTATCTCGCAATTAC 2854
 Db 100887 CTAATGTTGAAGTCTCGGCCAGTTTGTCTTTGAAGTTCGTGATCTCAGCGATTAT 100946
 QY 2855 AATGATAGCTTAGGAGCAAAATACCAATTCTA 2886
 Db 100947 AATGATAGCTTTGGGGTAAAGTTCCTCAATCTTA 100978

RESULT 9

AX06817
 ID AAX06817 standard; DNA; 2815 BP.
 XX
 AC AAX06817;
 XX

DT 26-APR-1999 (first entry)
 XX

DE Chlamydia pneumoniae surface exposed protein Omp5 DNA.

XX
 KW Omp5; outer membrane protein 5; surface exposed protein; antigen;
 XX infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
 XX

OS Chlamydia pneumoniae.

PH Key Location/Qualifiers
 CDS 1..2787
 FT /*tag= a
 TT

XX WO9858953-A2.

XX 30-DEC-1998.

XX 19-JUN-1998; 98WO-DK00266.

XX 23-JUN-1997; 97DK-0000744.

XX (BIRK/) BIRKELUND S.

(CHRI/) CHRISTIANSEN G.

Birkelund S, Christiansen G, Knudsen K, Madsen A;
 Mygind P;

WPI; 1999-105610/09.

P-PSDB; AAW88418.

Species-specific test for identifying mammals infected with
 Chlamydia pneumoniae - comprises detecting antibodies specific for
 outer membrane proteins of C. pneumoniae or nucleic acids encoding
 these proteins

Claim 6; Page 42-43; 115pp; English.

This DNA sequence codes for the novel 97.2 kDa surface exposed
 protein Omp5 (see AAW88418) of the human respiratory pathogen
 Chlamydia pneumoniae. By generating antibodies against C.
 pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
 was obtained which reacted with outer membrane proteins. The
 antibody was used to identify the genes (see AAX06816-27) encoding
 Omp4-Omp15 proteins (see AAW88417-28) in an expression library of
 C. pneumoniae DNA. The genes are situated in 2 gene clusters;
 Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
 the other, and encode polypeptides of about 89.6-100.3 kDa and
 about 56.1 kDa. The invention provides a new species specific test
 for identifying mammals (including humans) infected with Chlamydia
 pneumoniae. The test comprises detecting antibodies specific for
 Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
 membrane proteins, especially by PCR. The proteins are also used
 in the diagnosis of C. pneumoniae infection in mammals. The
 nucleic acids and proteins can also be used in the immunization of
 mammals, the nucleic acids being particularly useful as DNA
 vaccines for effecting in vivo expression of antigens. The
 vaccines may also prevent atherosclerosis and bronchial asthma,
 which are possibly associated with C. pneumoniae.

Sequence 2815 BP; 790 A; 575 C; 626 G; 824 T; 0 other;

Query Match 17.7%; Score 530.2; DB 20; Length 2815;
 Best Local Similarity 52.9%; Pred. No. 1.5e-136;
 Matches 1415; Conservative 0; Mismatches 1183; Indels 75; Gaps 10;

QY 247 TGCTGGAACCTACCTATTTTAAAGGGAATGTCACTCTAGAAAATATCTCTGGAACAGG 306
 Db 156 TACTGGAATAGCTATCTACTCTGACAGAGATATATCTCTGCAAAACCTTGGGATTCGG- 214
 QY 307 CACAGCAATCAAAAAGCTGTTTTTAAACAACATAAGGGCGATTTGACTTTTCAGGTAA 366
 Db 215 --CAGCTTTTAAAGGAGGGTGTGTTTCTGACACTACCGAATCTTTAAGCTTTGCGGTAA 272
 QY 367 GGGGAACCTCTCTATTGTTTCCAAACGGTGGATGACGGGACTGTAGCAGGGGCTCTGTAA 426
 Db 273 GGGGACTCACTTTCTTTTAAATATATAGTCTAGTCTGAGGCGCAGCACTTTCTGT 332
 QY 427 CAGCAGCGTGTAGATAAATCTACACGTTTATAGGGTTTTCTTCGCTATCTTTTATTC 486
 Db 333 TACAACCTGATAAAAATCTGTCGCTAACAGGATTTTCGAGTCTTACTTTCTAGCGGCC 392
 QY 487 GTCTCTCGGAAGTTCGATACTACCGGCAAGGAGCGTTAGCTCTCTACGGGTAGCTT 546
 Db 393 ATCATCGGTAATCAACCCCTCAGGAAAGGTCAGTTTAAATGTGGAGGGATC---T 449
 QY 547 GAGTTTGCAAAAAATGTGCTTTTCTTCAAGCAAAACCTTTTCAACGGATAATGCGGG 606
 Db 450 TACATTTGATCAATGGAATCTTTTATTTAAACAAGATTAATCTGTGAGGAAATGCGGG 509
 QY 607 TGCTATCACCGCAAAACTCTTTTCAATTAACAGGAGCTACAAATGTACAGCTCTGTTCGTA 666
 Db 510 AGCCCAATTTCTACCAAGAAATCTTTCTTTTGAAGAAACAGACCGGATCGATTTCTTTGAAGG 569
 QY 667 AAATA-----CCTCCTCAAGAAAGGCGGAGCCATTTCAGACTTCGATCCCTTAC 717

Db 570 GAATAAATCGAGCGCAACAGGAAAAAGGTTGGGCTATTGTGCTACTGGTACTGTAGA 629
Qy 718 CATTACTGGAACCAAGGGAAGTCTCTTTTCTGACAAATACTCTTTCCGGATTCGGAGC 777
Db 630 TATTACAATAATACGGCTCTACCTCTTCTGACAAATATCTGTAAGCTGAGGTGG 689
Qy 778 TGCAATTTTACAGAAAGCTCGGTGACTATTCTTAATATCTGTAAGTTTCTTTATTGA 837
Db 690 AGCTATAAATAGACAGGAAATCTGTAACAATACAGGAATACGTCTCTGTATTTTCTGA 749
Qy 838 CAATAAGGTCACAGGAGCGAGCTCTCTCAACAAACGGGGGATATGTCAGAGGTGCTACTG 897
Db 750 AAATAGTGTGAC---AGCGACCGAGGAAATGAGAGAGCTCTTCTGAGATGCC--- 802
Qy 898 TGCTTATAAATAGTACAGATTAAGTCACTCACTGACCTCTCACTGAAATCAGATGTTACTCTT 957
Db 803 -----ATGTTACCATATCTCGGAATCAGAGTGAACCTT 836
Qy 958 CAGCAACAATACATCAGCAACAGCGGAGAGCTATCTATGTGAAAAGCTCGAACTGGC 1017
Db 837 CTCAGGAAACCAAGCTGTAGCTAAATGGCGAGCCATTTATGCTAAGAAAGCTTACACTGGC 896
Qy 1018 TTCGGAGGACT-----TACCCTATTCACTAGAAATAGTGTCAATGAGGTACAGCTCC 1071
Db 897 TTCGGGGGGGGGGGGGTATCTCCTTTTCTAACAAATATAGTCCAGGTACCATCCAGG 956
Qy 1072 TAAAGTGGAGCCATAGCTATCGAAGATAGTGGGAAATGAGTTTATCCGCCGATAGTG 1131
Db 957 TAATGGTGGAGCCATTTCTATCTGCGAGCTGGAGGTGTAGTCTTTTTCAGCAGAGCAGG 1016
Qy 1132 TGCAATGTCTTTTAGGGAATACAGTCACTCTCTACTCTCC---TGGGAGCAATAGAG 1188
Db 1017 GGCAATTTACCTTCAATGGGAAATGCCAATGTTGCCAATCTACCAAACTACAAAAGAA 1076
Qy 1189 TAGTATCGACTTAGSAAACAGTGCAGAAATGACAGCTTTGGGTTCTGCTGTGTAGAGC 1248
Db 1077 TTCTATTGCAATAGGATCTACTGCAAGATCAAGAAATTAACGTGCAATATCTGGGCATAG 1136
Qy 1249 CATCTACTCTGTATGCCAATCTACTAGGATCATCCAAACAGTTACAGATGTTCTTAAA 1308
Db 1137 CATCTTTTCTAAGATCCGATTTACTGCTAATAGGCTGGGATTTCTACAGATCTTTAAA 1196
Qy 1309 AGTTAATGACTCCCGCAGATTTGCACTACAAATATACAGGAACATCATCTTCAAGG 1368
Db 1197 TCTCAATAAGGCTGATGAGGATTAATAGTACAGATTAATAGTGGTCTGATTTTCTGG 1256
Qy 1369 AGAAAAGTATCAGAGACAGGCGCAGATTTCTAAAATCTTACTTCCGAGCTACTACA 1428
Db 1257 TGAAGAAGCTCTTGAAGATGAACAAAGTTGACAGACACTCATCTTCTACGCTGAGCA 1316
Qy 1429 GCCTGAATCTTTACGAGGATCTCTATCTTTTAAACATGAGAGTGACTCTGACAGCTCA 1488
Db 1317 GCCTGTAACTTAACTGACAGGAATTTAGTACTTAAACGTGTGTGCTCTCGATACGAA 1376
Qy 1489 GGCAATTCACATCAACAGGAGATCTCGTCTCGAAATGGAGCTAGGAATCTACTCTAGAACC 1548
Db 1377 AGGCTTTACTCAGACCGGGTTCTCTGTATTATGAGTGGGCAACAGTTAAAAGC 1436
Qy 1549 ---TGCTGATCTAGAACCAATTAACAAATTTGGTCAATTAACATCATGTTCTATAGAGGTGC 1605
Db 1437 AAGTACAGAGAGGTCTATTAAAGGTCTTTTCAATCTCTGTAGACTCTTTAGGCGAGGG 1496
Qy 1606 AAAGAAAGCAAAATAGAAAACCAAGCTACGTCAAAAAATCTGATTTATCTGGAACCAT 1665
Db 1497 TAGGAAGTCTGTAATGCTCTCTGCGAGCAAGTAAATAGTCCCTTAGTGGTCCGAT 1556
Qy 1666 CACTTTATGACCCGAGCGGAGCTTTTATGAAAATCATAGTTTAAAGAAATCTCTCAGTC 1725
Db 1557 TCCTCTTTTGGATAACCAAGGGAATGCTTATGAAAATCAAGCTTAGGAAAACCTCAAGA 1616
Qy 1726 CTACGACATCTTAGAGCTCAAAGCTTCTGGAACTGTAAACAGCACCGAGTCACTCCAGA 1785
Db 1617 CTTTTCATTTGTGAGCTCTCTGCTCTGGGTCTGCGAACAATACAGATGTTCCAGCGGT 1676

Qy 1786 TCTTATAATGGGTGAGAAATTCATTTACGGCTATCAGGAACTTGGGCCCAATTTGTTG 1845
Db 1677 TCTTACAGTASCAACTCCTACGCACCTATGGGTATCAAGGTACTTGGGAAATGACTTGGGT 1736
Qy 1846 GG-----GGACAGGGGCTTTCTACGACTGCAACCTTCAACTGGACTTAAACCTGG 1893
Db 1737 TGATGATACCGCAAGCACTCCAAAGACTAAGACAGGACATTAGCTTGGACCAATACAGG 1796
Qy 1894 CTATATTCTTAATCCCGAGCTATCGGCTCTTTAGTCCCTAATAGCTTATGSAATGCAAT 1953
Db 1797 CTACCTTCCGAATCTGAGGCTCAAGGAGCTTTAGTTCCTAATAGCTTTTGGGGATCTTT 1856
Qy 1954 TATAGATATTAGCTCTCTCCATTTATTTGGAGACTGCAACAGGAGGTTGSCAGGGAGA 2013
Db 1857 TTCAAGCATCCAGCGATTTCAAGGTCTCATAGAGAGAGTGCTTTGACTCTTTGTTTCA 1916
Qy 2014 CCGTCTTTTGGTGTGCTGGATTTCTAACTTTCTTCCATAAGGATAGTACAAAACAGG 2073
Db 1917 TCGAGGCTTCTGGGCTGCGGGAGTCCCAATTTCTTTAGATAAGATAAGAAAGGGGAAAA 1976
Qy 2074 ACGGGGTTTTCGCCATTTGAGTGGGCTTATGTCTATAGGAGGAAACCTTACATCTTTGTT 2133
Db 1977 ACGCAATACCGTCAATAATCTGTTGATATGCTATCGAGGTGCGAGCAACTTTGTT 2036
Qy 2134 AGATAAGATTTCTAGTCTGCTCATTTTGTGAGCTCTTTTGAAGAGATAGAGACTACTTGT 2193
Db 2037 TGAATACTTAATAGCTTTTGGCTTTTGGCAACTCTTTTGTAGCTAAGATTTCTTAGT 2096
Qy 2194 AGCTAAGAAATCAAGGTGAGTCTACGAGGAACTCTCTATTACCAAGCAACCAACCTA 2253
Db 2097 CGCTAAAATCATACTGATACCTATGACGAGGCTTCTATATCCAAACATTTACAGATG 2156
Qy 2254 TATCTCTCTTCTTGGCAACTACGGCTTGTGTTGTTCTTATGTTCTTACAGATTC 2313
Db 2157 TAGTGGGTTCATAGGTTGTCTCTTAGATAAA---CTTCTGGCTCTTGGAGTCATAAAC 2213
Qy 2314 TGTTCTCTTTTTCAGGAAACCTTAGCTACACCAATACGGAATACGATCTGAAACCAAGTA 2373
Db 2214 CCTCTTTTGAAGCGGAGCTCGCTTATAGCCAGCTCAGTAATGATCTGAGACAAAGTA 2273
Qy 2374 TACAACATATCTACTCTTAAAGGAAGCTGGGGAAATGATGTTTTCGTTTGAATTCGG 2433
Db 2274 TACTCGGTATCTGAGGTGAAGGTTCTTGGGGAAATATGCTTTTAAATGATGTTGG 2333
Qy 2434 TGAAGAGCTCCGATTTGCTTAGATGAAGTGTCTATTGAGCAGTACATGCCCTTCAT 2493
Db 2334 AGCTTCTCTCATCTTATCTGAAATACCTGCAATGTTTGTATACCTATGCTCCATACAT 2393
Qy 2494 GAAATTCGAGTTTGTCTATGCACATCAGAGGTTTAAAGACAGGACAGAGCTCG 2553
Db 2394 CAACTGAATCTGACCTATATACCTCAGGACAGCTTCTCGAGAAAGGTACAGAGGAG 2453
Qy 2554 TGAATTTGGAAGTACCGGTCTTGAATCTTGCTTACCTATCGGATCCGATTTGATTA 2613
Db 2454 ATCTTTTGAATGACAGCACTCTTCAATTTATCTTTCCTATAGGGGTGAAGTTTGA 2513
Qy 2614 GGAATCAGACTGCCAAGATCAACGATCAATCTTAACTCTTGTGTTTACTGTGATCTTCT 2673
Db 2514 GTTCTCTGATGTAATGATCTTTCTTATGATCTGACCTTATCTCTATGTTCTGATCTTAT 2573
Qy 2674 TCGTATTAACCCGAGCTGTACGAAACACTGCGAATTTAGCGGTGATTCCTTGGAAACCTT 2733
Db 2574 CGCAATGATCCAAATGCACTACAGCACTTGAATCAGCGAGGCTCTTTGGGAAACTTA 2633
Qy 2734 CGGTACGATTTGGCAGACAGCTTTAGTCTCTGTCAGGGAACCAATTTTGTCTTAA 2793
Db 2634 TGCCATTAATCTAGCAACAGGCTTTCAGGTGCGTGCAGGAGCTCATCTAGCCCTTCTC 2693
Qy 2794 CTCAAATTTGAAGCTTTTAGCCAAATTTCTTTTGAATTCGTTGGGTCTCTCGCAATTA 2853
Db 2694 TCCTATGTTGAAGTGTGCGCCAGCTTGTCTTTGAAGTTTCTGTTGATCTCTACCGGATTA 2753

QY 2854 CAATGTAGACTTAGGACCAAAATACCAATTCTA 2886
 Db 2754 TAATGTAGATCTTGGGGTAACTTCCAAATTCTA 2786

RESULT 10

ABL91231
 ID ABL91231 standard; DNA; 2787 BP.

AC ABL91231;
 XX

DT 29-JUL-2002 (first entry)
 XX

DE Chlamydia pneumoniae cp0010 ORF DNA, SEQ ID NO:96.
 XX

XX Chlamydia pneumoniae; antigen; immunogen; vaccine; diagnosis;
 KW human respiratory disease; cardiovascular disease; atherosclerosis;
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
 KW strain CML029; open reading frame; ORF; gene; ds.
 XX

OS Chlamydia pneumoniae.
 XX

XX Key Location/Qualifiers
 FH CDS 1..2787

FT /tag= a
 FT /product= "cp0010"

FT sig_peptide 1..75
 FT /tag= b

FT mat_peptide 76..2784
 FT /tag= c

FT /product= "Mature protein"
 FT

XX WC020202606-A2.
 PN

XX 10-JAN-2002.
 PD

XX 03-JUL-2001; 2001WO-JB01445.
 XX

XX 03-JUL-2000; 2000GB-0016363.
 PR

XX 11-JUL-2000; 2000GB-0017047.
 PR

XX 21-JUL-2000; 2000GB-0017983.
 PR

XX 07-AUG-2000; 2000GB-0019368.
 PR

XX 18-AUG-2000; 2000GB-0020440.
 PR

XX 14-SEP-2000; 2000GB-0022583.
 PR

XX 10-NOV-2000; 2000GB-0027549.
 PR

XX 22-DEC-2000; 2000GB-0031706.
 PR

XX (CHIR-) CHIRON SPA.
 PA

XX Ratti G, Grandi G;
 XX

XX WPI; 2002-154726/20.
 DR

XX N-PSDB; ABB90573.
 DR

XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes -
 XX

XX Claim 5; Page 88-89; 364pp; English.
 PS

XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CML029), and ABL91184-ABL91173 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is
 CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of

CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
 CC the invention.

XX Sequence 2787 BP; 785 A; 568 C; 619 G; 815 T; 0 other;
 SQ

Query Match 17.6%; Score 527; DB 24; Length 2787;
 Best local Similarity 52.9%; Pred. No. 1.2e-135;

Matches 1413; Conservative 0; Mismatches 1185; Indels 75; Gaps 10;

QY 247 TGCTGGAATACCTACCTATTTAAAGGGAATGTCACTCTAGAAAATATTTCTGGAAACAGG 306

Db 156 TACTGGAATAGACTATCTCTGACAGGAGATATAAATCTGCAAAACCTTGGGATTCGG- 214

QY 307 CACGCAATCAAAAAGCTGTTTAAACACACTAAAGGGGATTTGACTTTTCACAGTAA 366

Db 215 --CAGCTTTAAGGAGGGTGTGTTTTCGACACTACGGAATCTTTAAGCTTTGCGGTAA 272

QY 367 CGGGAACCTCTATTGTTTCAAAACGTTGGATGACAGGACTGTAGCAGGGCTGCTGTAA 426

Db 273 GGGGTACTCACTTCTCTTTTAAATATTAAGTCTAGTGTGAAGGCGCAGCACTTCTGT 332

QY 427 CAGCAGCTGTAGTAAATCTACCACTTTATAGGGTTTCTTCGCTATCTTTATTC 486

Db 333 TACAACTGATAAAATCTGTCGTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCC 392

QY 487 GTCTCTCGAAGTTCGATAACTACCGCAAGAGGCGTGTAGCTCTACGGGTAGCTT 546

Db 393 ATCATCGGTATCAACACCCCTCAGGAAAAGTTCGATTAATGTGGAGGGATC---T 449

QY 547 GAGTTTGACAAAATGTCAGTTGCTCTTCAGCAAAAACCTTTTCAACGGAATATGCGG 606

Db 450 TACATTTGATAACAATGGAATCTTTTATTAACAAGATTTACTGTGAGAAAATGCGG 509

QY 607 TGCTATCACCGCAAAAACCTCTTTCATTAACAGGACTACATATGTCACTCTGTTTCTGA 666

Db 510 AGCCATTTCTACCAAGATCTTCTTTGAAAAACAGCACGGGATCGATTTCTTTGAGG 569

QY 667 AATA-----CCTCTCAAAAGAGCGGAGCCATTACAGACTTCGAGTCCGCTTAC 717

Db 570 GAATAAATCGAGCGCAACAGGGAAGGTTGGGGCTATTATGTCTACTTGTGACTGTAGA 629

QY 718 CATTACTGGAACCAAGCGGAGTCTCTTTTCTGCAATACTTCTTCGGAATCTGAGC 777

Db 630 TATTACAAATATACGGTCTCTACCTCTTCTGAAACAAATATCTGAGCTGAGGTGG 689

QY 778 TCGAATTTTACAGAACCTCGGTGACTATTCTTAATAAGCTAAAGTTTCTTTATTGA 837

Db 690 AGCTATAAATAGCACAGAAACTGTACAATTTACAGGGAATACGTCTCTGTATTTCTGA 749

QY 838 CAATAAGGTTCAGGAGCGAGCTCTCAACAACGGGGATATGTACAGAGGTGCTATCTG 897

Db 750 AATATAGTGTAC---AGCGACCGAGGAATGAGGAGCTCTTTCTGGAGATCGCG--- 802

QY 898 TGCTTTAAATAGTACAGATACTTAAGGTCACTCCCTCAGTGAATCAGATGTTTACTCTT 957

Db 803 -----ATGTTACCATATCTCGGAATCAGAGTGTAACTTT 836

QY 958 CAGCAACATATACATCGAACACAGCGGAGAGCTATCTATGTGAAAAAGCTCGAATCGG 1017

Db 837 CTCGGAACCAAGCTGTAGTAAATGCGGAGCCATTATGCTAAGAAAGCTTACRCTGGC 896

QY 1018 TTCCGGAGGAC-----TTAGCCCTATTTCAGTAGAAATAGTCTCAATCGAGGATCAGCTCC 1071

Db 897 TTCCGGGGGGGGGGGTATCTCTTTTCTAACAATATAGTCCCAAGTACCCTGAGG 956

QY 1072 TAAAGGTGAGCCATAGCTATCGAAGATAGTGGGGAATTTAGTTTATCCGCGGATAGTG 1131

Db 957 TAATGGTGGAGGCATTTCTTACTGCGAGCTGGAGAGTGTAGTCTTTTTCAGCAGAAGCAGG 1016

QY 1132 TGACATTGTCTTTTATAGGGAATACAGTCACTTCTACTACTCC---TGGGACGAATAGAAG 1188

Db 1017 GGACATTACCTTCAATGGGAATGCCATTTCTGCAACTACACCAAACTACAAAAGAAA 1076
 QY 1189 TAGTATCGACTTAGGAACGAGTGCAGAGATGACAGCTTTGCTTCTGCTGCTGGTAGAGC 1248
 Db 1077 TTCTATTGACATAGGATCTACTGCAAGATACGAATTTACGTGCAATATCTGGGCATAG 1136
 QY 1249 CATCTACTTCTATGATCCCATTAACCTACAGGATCATCCCAACAGTTACAGATGCTCTAAA 1308
 Db 1137 CACTCTTTTCTAGATCCGATTTACTGCTAATACGGCTGGGATTTCTACAGTACTTTAAA 1196
 QY 1309 AGTTATAGACCTCCGCGAGATTTCTGCACCTAAATATACAGGGAACATCATCTTCACAGG 1368
 Db 1197 TCTCAATAAGGCTGATGCGAGGTAATAGTACAGATTTATAGTGGGTGCGATTTGTTTTCTGG 1256
 QY 1369 AGAAAAGTTATCAGAGACAGAGCCGAGATTTCTAAAAATCTTACTTCCGAAGCTACTACA 1428
 Db 1257 TGAAGAGCTCTGAGAGATGAAGCAAAAGTTGAGACAACTTCACTTCTACGCTGAAGCA 1316
 QY 1429 GCTGTAACTCTTTAGGAGGTACTCTCTATCTTTAAACATGGAAGTACCTCTGCAGACTCA 1488
 Db 1317 GCCTGTAACTCTAACTGCGAGGAAATTTAGTACTTAAACGCTGGTGTCACTCTCGATACGAA 1376
 QY 1489 GGCATTCACTCAACAGCGAGATTTCTCGTCTCGAAATGGAAGTGAAGAACTACTCTAGAACC 1548
 Db 1377 AGCTTTTCTCAGACCGCGGTTCTCTGTTATATAGATGCGGCACAAAGTTTAAAGC 1436
 QY 1549 ---TGCTGATPACAGACCATAAACAAATTTGTCATTAACATCAGTTCTATAGACGGTGC 1605
 Db 1437 AAGTACAGAGGAGGTCACTTTAACAGGCTTTTCCATTTCTGTAGACTCTTTTAGGCGAGGG 1496
 QY 1606 AAGAAGGCAAAATAGAACCAAACTAGCTCAAAATCTGACTTTATCTGGAACCT 1665
 Db 1497 TAAGAAGTTGTAATTTGCTCTTCTCAGCAAGTAAATATGAGCCCTTAGTGGTCCGAT 1556
 QY 1666 CACTTTATTTGACCCGAGCGGACGTTTATGAAAATCATAGTTTAAAGAAATCTTCAGTC 1725
 Db 1557 TCTTCTTTTGATAAACCAAGGAATGCTTATGAAAATCAAGCTTAGGAAAACCTCAAGA 1616
 QY 1726 CTAGGACATCTTAGACCTCAAGCTTCTGGAAGTGAACAGACCGGAGTACTCCAGA 1785
 Db 1617 CTTTTCATTTGTGACGCTCTGCTCTGGGTACTGCAACACTACAGATGTTTCCAGCGT 1676
 QY 1786 TCCTATAATGGGTGAGAAATTCATTAACGCTATCAGGAACTTGGGGCCCAATTTGTTG 1845
 Db 1677 TCCTACAGTAGCAACTCCTACGACATATGGGTATCAAGTACTTGGGNACTGACTGGGT 1736
 QY 1846 GG-----GGACAGGGGCTCTACGAGTGCACCTTCAACTGAGCTAAACCTGG 1893
 Db 1737 TGATGATACCGCAAGCACTTCAAGACTAAGACAGCGACATTAGCTTTGGACCAATACAGG 1796
 QY 1894 CTATATTTCTTAATCCCGAGGATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGCATT 1953
 Db 1797 CTACCTTCGAACTCTGAGGGTCAAGACCTTTAGTTCTTAATAGCTTTGGGGATCTTT 1856
 QY 1954 TATAGATATTAGCTCTCTCCATTTATCTTATGAGACTGCAAAAGAGGTTCCAGGGAGA 2013
 Db 1857 TTCAGACATCCAAGCGATTCAAGGTGTCTATAGAGAAAGTGTCTTGACTCTTTGTTTCA 1916
 QY 2014 CCGTGCTTTTGGTGTGCTGGATATCTAATCTTCCATAGGATAGTAGTACAAAACAGC 2073
 Db 1917 TCAGGGCTTCTGGGCTGCGGAGTGCCTCAATTTCTTAGATAAGATAAGAAAGGGGAAA 1976
 QY 2074 ACSCGGGTTTTCGCAATTTAGTGGCGGTTATGTCTATAGGAGGAAACCTTACATCTTTGTT 2133
 Db 1977 ACGCAATATACGTCATAAAATCTGTTGATATGCTATCGGAGTGCAGCGCAACTTTGTT 2036
 QY 2134 AGATAAGATTTCTAGTCTGCATTTTGTCTAGCTCTTTTGAAGAGATAGAGACTATTTGT 2193
 Db 2037 TGAAGACTTAATAGCTTTTGGCTTTTGGCAACTCTTTTGGTAGCGATAAAGATTTCTTAGT 2096
 QY 2194 AGCTAAGAACTCAAGGTACAGTCTACGAGGAACTCTCTATTACGACCAACGAAACCTTA 2253

Db 2097 CGCTAAAAATCATACTGATACCTATGACGAGGCTTCTATATATCCAAACATTACAGAATG 2156
 QY 2254 TATCTCTCTCTCTTGCABAACTACGGCTTGTTCGTTGTCTTATGTTCCTACAGATTC 2313
 Db 2157 TAGTGGGTTCTATAGTGTGTCTTTAGATAAA---CTTCTGGCTCTTGGAGTCATAAAAC 2213
 QY 2314 TGTTCCTTTTTCAGGAAACCTTTAGCTTACACCCATACGGAATAACGATCTGAAAACCAAGTA 2373
 Db 2214 CCTCGTTTTAGAAGGCGAGCTCGCTTATAGCCACGTCAGTAAATGATCTGAGACAAAGTA 2273
 QY 2374 TACAACATATCTCTACTGTTTAAAGGAAGCTGGGGATGATAGTTTCGCTTTAGAAATCGG 2433
 Db 2274 TACTGGGTATCTCTGAGGTGAAAGGTTCTTGGGGGAATAATGCTTTTAAACATGATGTGG 2333
 QY 2434 TGAAGAGCTCCCATTTGCTTTAGATGAAAGTGCTCTATTTTGAGCAGTACATGCCCTTCAT 2493
 Db 2334 AGCTTCTCTCTCATCTTATCTCTGATACCTGATTTGATACCTATGCTCCATACAT 2393
 QY 2494 GAAATTCAGTCTTGTCTATGACATCAGGAAGGTTTAAAGAACAGGGAACAGAGCTCG 2553
 Db 2394 CAAACTGAATCTGACCTATATAGCTCAGACAGCTTCTCGGAGAAAGGTACAGAAAGGAG 2453
 QY 2554 TGAATTTGGAAGTAGCGCTTCTGTGAATCTTGTCTTACCTATCGGATCCGATTTGATAA 2613
 Db 2454 ATCTTTTGTAGCAGCAACCTCTTCAATTTATCTTTGCCCTATAGGGTGAAGTTTGAGNA 2513
 QY 2614 GGAATCAGACTGCCAAGATGCAACGTAACATCTAATCTTGTGTATACCTGTGATCTTGT 2673
 Db 2514 GTTCTCTGATTTGATGACTTTTCTTATGATCTGACTTTATCTTATGTTCTCTGATCTTAT 2573
 QY 2674 TCGTAGTAACCCCGACTGTACGACAACTGCGAATTAGCGGTGATTTCTTGGAAAACCTT 2733
 Db 2574 CCGCAATGATCCCAATGACACTACAGCACTTGTATATCAGCGAGCTCTTGGGAAACTTA 2633
 QY 2734 CGGTAGCAATTTGGCAAGCAAGCTTTAGTCTCTCGTGCAGGGAACCAATTTTGTCTTAA 2793
 Db 2634 TGGCAATAACTTAGCAGCAGCGCTTGCAGTGTGCGAGGCTACACTACGCTTCTC 2693
 QY 2794 CTCAAATTTTGAAGCTTTTAGCCAAATTTCTTGTGATTTGCTGGGTCTATCTCGCAATTA 2853
 Db 2694 TCCTATGTTTGAAGTGTCTCGGCCAGTGTCTTGTGAGTTCGTGATCTCTCAGGATTTA 2753
 QY 2854 CAATGTAGACTTAGGAGCAAAATACCAATTTCTA 2886
 Db 2754 TAATGTAGATCTTTGGGTAAGTTCCCAATTTCTA 2786
 RESULT 11
 ID AA261509 standard; DNA; 2957 BP.
 XX AA261509;
 AC AA261509;
 XX 19-JUN-2000 (first entry)
 DT DNA encoding the CPN100395 polypeptide.
 DE CPN100395; Chlamydia infection; immune response; vaccine; ss.
 KW Chlamydia pneumoniae.
 OS Chlamydia pneumoniae.
 XX Key Location/Qualifiers
 FH CDS 101..2857
 FT /*tag= a
 XX WO200011183-A2.
 PN 02-MAR-2000.
 PD 18-AUG-1999; 99WO-1B01449.
 XX 20-AUG-1998; 98US-0097187.
 PR 20-AUG-1998; 98US-0097188.
 PR

Db 1775 CTAATACATCACTACTGATGATCAAGGAACCTGGAATATTGTTGGTCCGACAT 1834
 QY 1847 GGGACAGGGCTTCTACGACTGCAACCTTCACTGGACTAACTGGCTATATTCCTAAT 1906
 Db 1835 GCAATGCAAAACAAAATGCTACCTTAATCTGGACTAAACAGGATCAAGCCGAAT 1894
 QY 1907 CCGAGCGGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGATATATAGC 1966
 Db 1895 CCAGAACGTCAGGACCTTTGGTCTCTAATAGCTTGTGGGTCTTTGTGATGTCGC 1954
 QY 1967 TCTCTCAATATCTATGAGAGCTCAACAGAGGTTGCGAGGAGACCGTCTTTTGG 2026
 Db 1955 TCCATTTCAGAGCTCATGGACCGGACACAAATTCGTTATCTTCGTCAACAATTTTGG 2014
 QY 2027 TGTGCTGATATCTAACTTCTTCCATAAGGATAGTCAAAAACAGACGCGGTTCGC 2086
 Db 2015 GTATCAGGATCGCGACTTTTGTGATGAGATCAGAAAGGAAACCAACGATGATCGT 2074
 QY 2087 CATTTGAGTGGCGTTATGTCATAGGAGAAACCTTACATATCTTGTTCAGATAAGATCTT 2146
 Db 2075 CATTCAGCGGGTTATGCAATAGGAGGAGGATTCCTTACGGCTTCTGAAATTTCTTT 2134
 QY 2147 AGTGTGCAATTTTTCAGCTCTTTCGAGAGATAGAGACTACTTGTAGCTAAGAACTAA 2206
 Db 2135 AATTTTGTCTTTTGTGACGCTTTTGTGCTACGACAGGACCACTTGTGGCTAAGAACCA 2194
 QY 2207 GGTACAGTCTACGAGGAACCTCTTATTTACCAGCACAAACCACTATATCTCTCTTCT 2266
 Db 2195 ACCATGATATATGAGGGCAATAGTTTACGACACCTCGGAGAGTCTAAGACCTCGCT 2254
 QY 2267 TCGAACTACGCGCTTGTGCTGTCTTATGTTCTTACAGAGATTCCTGTTCTCTTTTCA 2326
 Db 2255 AAGAT-----TTTGTGAGAAATCTTGACTCCCTACCTTTTGTCTTCAAT 2299
 QY 2327 GGAACCTTAGCTACACCATACGATACGATACGATACGATACGATACGATACGATACCT 2386
 Db 2300 GCTCGTTTGTCTTATGCGCATACGACATACATATGATGACCAAGATACCTGGCTATCT 2359
 QY 2387 ACTGTTAAAGAGCTGGGGGAATGATGTTTGGCTTTAGAAATCGGTGGAAGAGCTCCG 2446
 Db 2360 CCGTTTAAAGGAAGCTGGGGAATGATGCTTGGGTATAGAAATGAGGAGGAGCTATCCG 2419
 QY 2447 A--TTTGTGATGAAAGTCTCTATTTGAGCAGTACATGCTTCTCATGAATTCGAG 2503
 Db 2420 GTAGTTGCTTCAGGAGCTGCTTGGTGGTATCCACACCCATTTCTAACTAGAG 2479
 QY 2504 TTTGTCTATGCATCAGGAAGTTTAAAGAACAGGGAACAGAGCTCGTGAATTTTGA 2563
 Db 2480 ATGATCTATGCATCAGAAATGACITTAAGGAAACCGCAGAGAGCGGTTCTTCCAA 2539
 QY 2564 AGTAGCGCTTGTGATCTTGCCTTACCTATCGGGATCCGATTTGATAGGAATCAGAC 2623
 Db 2540 AGTGAAGACCTTCTCAATCTAGCGTCTCTGAGGATAAATTTGAGAA-----ATTC 2593
 QY 2624 TGCAGAGTGCACATACATCTTCTGTTTATCTGTTGATCTTGTGCTGATGATTAAC 2683
 Db 2594 TCCGATAGCTCTAGTATGATCTCTCCATAGCTTACGTTCCGATGCTGATTCGTAATGAT 2653
 QY 2684 CCGACTGTACGACAACTGCGAATAGCTGATCTTGTGAAACCTTCGGTACGAAAT 2743
 Db 2654 CCAGGCTGCACGACAACTCTTATGTTTCTGCGGATCTTGTGTCACATGTTGGTACAGC 2713
 QY 2744 TTGGCAAGACAGCTTATGCTCTTGTGCGAGGACCAATTTTGTCTTAACTCAATTTT 2803
 Db 2714 TTGCTAGACAGCTCTTCTGATGCTGCGAATCAATGATGCTTGTCTTCAACTTT 2773
 QY 2804 GAAGCCTTTAGGCAATTTCTTTGAATTCGTTGGGTCTATCTCGCAATTACAAATGAGAC 2863
 Db 2774 GAAGTTTTCAGTCAGTTTGAAGTCGAGTTTGCAGGTTTCTTCTCGTAGCTATGCTATCGAT 2833
 QY 2864 TTAGGAGCAAAATACCAATTTCTAATGC 2890
 Db 2834 CTTGGAGGAAGATTCGGATTTTAAATCC 2860

RESULT 12

ABL91192
 ID ABL91192 standard; DNA; 534 BP.

XX
 AC ABL91192;

XX
 DT 29-JUL-2002 (first entry)

XX
 DE Chlamydia pneumoniae cp0014 ORF DNA, SEQ ID NO:18.

XX
 KW Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
 human respiratory disease; cardiovascular disease; atherosclerosis;
 coronary artery disease; carotid artery stenosis; myocardial infarction;
 cerebrovascular disease; aortic aneurysm; claudication; stroke;
 strain CWL029; open reading frame; ORF; gene; ds.

XX
 OS Chlamydia pneumoniae.

XX
 FH Key Location/Qualifiers
 CDS 1..534
 FT /*tag= a
 FT /product= "cp0014"

XX
 PN WO200202606-A2.

XX
 PD 10-JAN-2002.

XX
 PF 03-JUL-2001; 2001WO-IB01445.

XX
 PR 03-JUL-2000; 2000GB-0016363.

XX
 PR 11-JUL-2000; 2000GB-0017047.

XX
 PR 21-JUL-2000; 2000GB-0017983.

XX
 PR 07-AUG-2000; 2000GB-0019368.

XX
 PR 18-AUG-2000; 2000GB-0020440.

XX
 PR 14-SEP-2000; 2000GB-0022583.

XX
 PR 10-NOV-2000; 2000GB-0027549.

XX
 PR 22-DEC-2000; 2000GB-0031706.

XX
 PA (CHIR-) CHIRON SPA.

XX
 PI Ratti G, Grandi G;

XX
 DR WPI; 2002-154726/20.

XX
 DR N-PSDB; ABB90534.

XX
 PT Novel Chlamydia pneumoniae protein useful in the manufacture of a
 medicament for treatment or prevention of infection due to Chlamydia,
 preferably Chlamydia pneumoniae, and for diagnostic purposes -
 Claim 5; Page 49; 364pp; English.

XX
 CC Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
 them. The proteins are predicted to be immunogenic and may therefore be
 useful in vaccine production and for diagnostic purposes. Chlamydia
 pneumoniae is a common cause of respiratory disease in humans, and is
 also involved in the development of cardiovascular diseases such as
 atherosclerosis, coronary artery disease, carotid artery stenosis,
 myocardial infarction, cerebrovascular disease, aortic aneurysm,
 claudication and stroke. The proteins and nucleic acids of the invention
 may be used in vaccines and pharmaceutical compositions for the
 prevention or treatment of chlamydial infections, particularly Chlamydia
 pneumoniae infections. The proteins may also be used in the detection of
 Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 DNA probe assay or blotting techniques for determining Chlamydia
 pneumoniae gene expression. The present sequence represents a
 specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
 the invention.

XX
 SQ Sequence 534 BP; 147 A; 105 C; 117 G; 165 T; 0 other;

| | | |
|--|---|--|
| Query Match | | 17.4%; Score 523; DB 24; Length 534; |
| Best Local Similarity | | 99.8%; Pred. No. 6.8e-135; |
| Matches 534; Conservative 0; Mismatches 0; Indels 1; Gaps 1; | | |
| QY | 101 | ATGAAGTCTCTCTTCCCAAGTTGTATTTCTACATTTGCTATTTTCCCTTTGCTATG 160 |
| DB | 1 | ATGAAGTCTCTCTTCCCAAGTTGTATTTCTACATTTGCTATTTTCCCTTTGCTATG 60 |
| QY | 161 | ATTGCTACCGACAGTCTTGGATTCAGTGGAGTTTCGATGGGAATAAAATGGTAAT 220 |
| DB | 61 | ATTGCTACCGACAGTCTTGGATTCAGTGGAGTTTCGATGGGAATAAAATGGTAAT 120 |
| QY | 221 | TTTTCAAGTTCGAGAGTTCAGAGATCGGAAGATCTGGAATCTACCTATTTAAAGGGAATGTC 280 |
| DB | 121 | TTTTCAAGTTCGAGAGTTCAGAGATCGGAAGATCTGGAATCTACCTATTTAAAGGGAATGTC 180 |
| QY | 281 | ACTCTAGAAATATTCCTGGACAGGACAGCAATCAAAAAGCTCTTTTACCAACT 340 |
| DB | 181 | ACTCTAGAAATATTCCTGGACAGGACAGCAATCAAAAAGCTCTTTTACCAACT 240 |
| QY | 341 | AAGGCGGATTTGACTTTTCAAGGTAACGGGAACCTCTATTTGTTCCAAACGGTGGATGCA 400 |
| DB | 241 | AAGGCGGATTTGACTTTTCAAGGTAACGGGAACCTCTATTTGTTCCAAACGGTGGATGCA 300 |
| QY | 401 | GGGACTGTAGAGGGGCTGCTGTTTAAACAGGAGCTGTAGATAATCTACCACTTTATA 460 |
| DB | 301 | GGGACTGTAGAGGGGCTGCTGTTTAAACAGGAGCTGTAGATAATCTACCACTTTATA 360 |
| QY | 461 | GGGTTTCTTCGCTATCTTTTATTCGCTCTCTGGAAGTTCGATAAATACCGGCAAGGA 520 |
| DB | 361 | GGGTTTCTTCGCTATCTTTTATTCGCTCTCTGGAAGTTCGATAAATACCGGCAAGGA 420 |
| QY | 521 | GGCGTAGCTGTCTACCGGTAGCTTGAATTTGACAAAATGTCAGTTGCTCTTCAGC 580 |
| DB | 421 | GGCGTAGCTGTCTACCGGTAGCTTGAATTTGACAAAATGTCAGTTGCTCTTCAGC 479 |
| QY | 581 | AAAACTTTTCAACGGATAATGGCGTGTCTATCACCGCAAAAACCTTTTCAATAA 635 |
| DB | 480 | AAAACTTTTCAACGGATAATGGCGTGTCTATCACCGCAAAAACCTTTTCAATAA 534 |
| RESULT 13 | | |
| AA06821 | | |
| ID | AA06821 | standard; DNA; 2757 BP. |
| AC | AA06821; | |
| XX | | |
| XX | 26-APR-1999 | (first entry) |
| DT | | |
| DE | | Chlamydia pneumoniae surface exposed protein Omp9 DNA. |
| XX | | |
| XX | | Omp9; outer membrane protein 9; surface exposed protein; antigen; |
| KW | | infection; diagnosis; vaccine; atherosclerosis; asthma; ss. |
| XX | | |
| OS | | Chlamydia pneumoniae. |
| XX | | |
| PN | WO9858953-A2. | |
| XX | | |
| PD | 30-DEC-1998. | |
| XX | | |
| PF | 19-JUN-1998; 98WO-DK00266. | |
| XX | | |
| PR | 23-JUN-1997; 97DK-0000744. | |
| XX | | |
| PA | (BIRK/) BIRKELUND S. | |
| XX | | |
| PA | (CHR/) CHRISTIANSEN G. | |
| XX | | |
| PI | Birkelund S, Christiansen G, Knudsen K, Madsen A; | |
| PI | Mygind P; | |
| XX | | |
| DR | WPI; 1999-105610/09. | |
| XX | | |
| DR | P-PSDB; AA06822. | |
| XX | | |

Species-specific test for identifying mammals infected with Chlamydia pneumoniae - comprises detecting antibodies specific for outer membrane proteins of C. pneumoniae or nucleic acids encoding these proteins

Claim 6; Page 55-56; 115pp; English.

This DNA sequence codes for the novel 96.7 kDa surface exposed protein Omp9 (see AAW88422) of the human respiratory pathogen Chlamydia pneumoniae. By generating antibodies against C. pneumoniae outer membrane complex, a polyclonal antibody (PAB 150) was obtained which reacted with outer membrane proteins. The antibody was used to identify the genes (see AAX06816-27) encoding Omp4-Omp15 proteins (see AAW88417-28) in an expression library of C. pneumoniae DNA. The genes are situated in 2 gene clusters: Omp12, 11, 10, 5, 4, 13 and 14 in one cluster and Omp6, 7, 8, 9 and 15 in the other, and encode polypeptides of about 89.6-100.3 kDa and about 56.1 kDa. The invention provides a new species specific test for identifying mammals (including humans) infected with Chlamydia pneumoniae. The test comprises detecting antibodies specific for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae.

Sequence 2757 BP; 770 A; 564 C; 642 G; 781 T; 0 other;

Query Match 17.4%; Score 522.2; DB 20; Length 2757;

Best Local Similarity 53.4%; Pred. No. 2.5e-134;

Matches 1424; Conservative 0; Mismatches 1153; Indels 90; Gaps 12;

| | | |
|----|-----|---|
| QY | 242 | GAAGATGCTGGAACCTACCTATTTAAGGGAATGTCACTCTAGAAAATATTCCTCGA 301 |
| DB | 160 | GATGCTAGTGGACAGACCTATATTCGTGGGATGTCTGATA---AGCCAGCAGGG 216 |
| QY | 302 | CAGGCACAGCAATCAAAAAGCTGTTTAAACACTAAGGGCGATTTGACTTTCACA 361 |
| DB | 217 | AAACAAACGAGCTTAACCAAGTTGTTTTTCTAACACTGCAGGAATCTTACCTCTTA 276 |
| QY | 362 | GGTAACGGGAACCTCTATTTGCCAAACGGTGGATGCAGGACTGTAGCAGGGGTGCT 421 |
| DB | 277 | GGGAACGGAATTTCTTTCATTTTGACAAATATTTTCTGCTACTGTGAGGTGTGTT 336 |
| QY | 422 | GTTAACAGCAGCGTGTGTAGATAAATCTACACGTTTATAGGGTTTCTTCGCTATCTTT 481 |
| DB | 337 | GTTAGCAATACAGCAGCTTCTGGGATTACGAAATTTCTCAGGATTTTCAACTCTTCGGATG 396 |
| QY | 482 | ATTGCTCTCTCGGAAGTTTCGATAACTACCGCAAGAGCGGTAGCTGCTTACCGGT 541 |
| DB | 397 | CTTGAGCTCTCT-----AGNCCACAGGTAAAGAGCCATTA---AAATTCAGAT 444 |
| QY | 542 | AGCTTGAAGTTGACAAAATGTCTAGTTTGTCTTCAGCAAAAACCTTTTCAACGGATAAT 601 |
| DB | 445 | GGTCTGGTGTGAGAGTATAGGGAATCTTGACCAAAATGAAATGCTCTAGTGAAT 504 |
| QY | 602 | GGGGTGTCTACCGCAAAACCTTTTCAATTAACAGGAGTACAAATGCTAGCTCTGTT 661 |
| DB | 505 | GGGGGAGGCATCAATACGAAGCTTTGCTTGTAGCTGGAGTACCGGTTTGTAGCGTTC 564 |
| QY | 662 | TCTGAAAATACCTCTCTCAAGAAAGCGGAGCCATTCAGACTTCGATGCCCTTACCATT 721 |
| DB | 565 | CTTGCAATAGCTCTGTCACACAGGAGGAGGATCTATGCTTCTGGTACTCTGTGATT 624 |
| QY | 722 | ACTGGAACCAAGGGAGTCTCTTTTCTGACAAATCTTCTCGAATCTTGTGGAGTGC 781 |
| DB | 625 | TCTGGAATGTCAGGAATCTTGAAGCTTCGGAACCAACAGTGGGCAACATCAGGAGGCG 684 |
| QY | 782 | ATTTTTCAGAGAAGCCTCGGTGACTATTTCTTAATATGCTAAAGTTTCTCTTATTGCAAT 841 |

Db 685 ATCTCTGCTGAAGGAACCTTGTGATCTCCATAACCAAAATATCTTTTCGATGGCTGC 744
Qy 842 AAGGTACAGGAGCGAGCTCTCAACACGGGGATATGTACGAGAGGTGCTATCTGTGCT 901
Db 745 AAAGCAACTACAAATGGCGAGCTATTGAATGTAACAAAGCAGGGG-----790
Qy 902 TATAAACTAGTACAGATACAAAGTCAACCTCACTGGAAATCAGATGTTACTCTTCAGC 961
Db 791 -----CGAACCCAGACCTATCTTGACTCTTCAGGAAATGAGAGCGCTGCATTTCTG 843
Qy 962 AACATACATCGACAAACAGCGGAGAGAGCTATCTATGTGAAAAGCTGAACTGCTTCC 1021
Db 844 AATAACACAGCAGGAATAGTGAGGTGCAATTTATACCAAAAAATGGTGTTATCTCCA 903
Qy 1022 GGAGGACTTACCCCTATTAGTGAATAAGTGTCAATGGAGGTACAGCTCCTAAAGGTGA 1081
Db 904 GGCAGGAGGAGGTGTTATTTCTAACAAAGCTGCGAATGCTACTCTTAAGAGGG 963
Qy 1082 GCCATAGCTATCGAAGATAGTGGGAATTGAGTTTATCCCGGATAGTGGTGAATGTC 1141
Db 964 GCAATTTGCGATTCTAGATTCTGAGAGATTAGCAATTTCTGCAGATCTCGGCAATATCAT 1023
Qy 1142 TTTTATAGGATACAGTCTCTTAC-----TACTCTGGGACGATAGTAGTAGTATC 1195
Db 1024 TTCAGGGCAATACTACGAGCTACAGGAAGTCTCGAGTGTGACCGAATATGCTATA 1083
Qy 1196 GACTTAGGAACGAGTGCAGAGATGACAGCTTTGCTGCTGCTGGTAGAGCCATCTAC 1255
Db 1084 GATCTTGCATCGAATGCAAAATTTTAAATCTCGAGCGACTCGGGGAATAAAGTTAT 1143
Qy 1256 TTCTATGATCCCTAATACTACAGATCATCCACACAGATTACAGATGCTCTTAAAGTTAT 1315
Db 1144 TTCTATGATCCCTATACGA-----GCTCAGGAGCTACTGATAGCTCTCTTTGAT 1194
Qy 1316 GAGACTCCGCGACATCTGCATCTACATAATACAGGGAACATCATCTTCACAGAGAAAG 1375
Db 1195 AAAGCTGACGACGATCTGGMAATACCTATGAGGCTACATCGTTTCTCGGAGGAA 1254
Qy 1376 TTATCAGACAGAGCGCGAGATTCTAAATCTTACTTGGAGCTACTACAGCTGTA 1435
Db 1255 CTCTCAGAGAGGAACTTAAGAAACCTGACAACTCTGAAGTCTACATTTACACAGGCTGTA 1314
Qy 1436 ACTCTTTCAGAGGATCTCTATCTTAAACATGAGAGTACTCTGCAGACTCAGGCTTC 1495
Db 1315 GAGCTGCTCAGGTGCTTAGTATTGAAGATGAGTGTAGTGTAGTGTGCAATACTATA 1374
Qy 1496 ACTCAACAGCAGATCTCTGCTCGAAATGAGAGTACTACTCTAGA-----ACCTGT 1552
Db 1375 ACGCAGGTCGAGGATCGAAAGTCGTTATGATGGAGGAGTACTTTTCAGGCGAAGCGCT 1434
Qy 1553 GNTACTAGCACCATTAACAATTTGGTCAATTAACATCAGTCTTATAGACGCTGCAAGAG 1612
Db 1435 GAGGGGTCTACTCTCAATGGCTTAGCCATTAATATAGATTCTTATAGTGGACAATAAA 1494
Qy 1613 GCAAAAATAGAAACCAAGCTACGTCAAAAAATCTGACTTTATCTGGAAACCATCACTTTA 1672
Db 1495 GCTATCTAAGGCGAGCGCAGCAAGTAAGGATGTTGCTTTATCAGGGCTATCATGCTT 1554
Qy 1673 TTGACCCGAGCGGACGTTTATGAATCATAGTTTGAAGATCCTCAGTCTACGAC 1732
Db 1555 GTAGATCTCAGGGGAATATTATGAGCATATAATCTCAGTCAACAGCAGGCTTTCTCT 1614
Qy 1733 ATCTTAGAGCTCAAGGCTCTGGAACGTGAACAGACACCGAGTACTCCAGATCTCTATA 1792
Db 1615 TTAATAGAGCTTCTGCACAGGACGATGACTACTACATATCCCCGATACCCCAATT 1674
Qy 1793 ATGGGTGAGAAATTCATTAAGCTATCAGGAACTTGGGGCCCAATTTGTTGGGGACA 1852
Db 1675 CTAATACTACGAATCACTATGGGTATCAAGGAAC-----GGAATAATTTGTTGGGTCGAC 1731
Qy 1853 GGGGCTCT-----ACGACTGCAACCTTCACTGGACTAAACTGCTATATCTCT 1903
Db 1732 GATGCACTGCAAAAAACAAAAATGCTTACCTTAACTTGGACTAAACAGGATACAGCG 1791

RESULT 14

AAA30851

ID AAA30851 standard; DNA; 2950 BP.

Qy 1904 AATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGAATGCAATTTATAGATTT 1963
Db 1792 AATCCAGAACTCAGGACCTTTGGTCTCTAATAGCTGTGGGTCTTTTGTCTGATGTC 1851
Qy 1964 AGTCTCTCATTTATCTTATGGAGACTGCAAGAGAGGTTCGAGGAGACCGTCTTTT 2023
Db 1852 CGTCTCATTCAGAGCCTCATGACCGGAGCACAAGTTCGTTATCTTCGTCAACAAATTTG 1911
Qy 2024 TGTGTGCTGATTTATCTAATCTTCTCATAGTAGTACAAAACACAGCGCGGTTT 2083
Db 1912 TGGGTATCAGAAATCGGAGCTTTTTCATGAGATCAGAAAGGAAACCAAGTAGTAT 1971
Qy 2084 CGCATTTGAGTGGCGGTTATGTATAGGAGGAACTCATACTATTGTTTCAGATAAGATT 2143
Db 1972 CGTCATTTAGCGCGGTTATGCAATTAGGAGGAGTCTTACGCGCTTCTGAAATTTTC 2031
Qy 2144 CTTAGTCTGCATTTTGTCTGAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAT 2203
Db 2032 TTTAAATTTTGTCTTTTGTCTGAGCTTTTGGCTACGACAGGACCATCTTGTGGCTAAGAAC 2091
Qy 2204 CAAGGTACAGTCTACGAGGAACTCTCTATTTACCAGCACAAAGAAACCTTATCTCTTT 2263
Db 2092 CATACCATGTATATGACAGGGCAATGAGTTACCGACACTCGAGAGTCTAAGACCTC 2151
Qy 2264 CTTTGGAACTACGGCCCTGTTCTGTTCTTATGTTCTTACAGAGATTCCTGTTCTCTTT 2323
Db 2152 GCTAAGA-----TTTTGTCAAGAAATTTCTGACTCCCTACCTTTTGTCTTC 2196
Qy 2324 TCAGGAAACCTTAGCTACACCCATACGATAACGATCTGAAACCAAGTATACACATAT 2383
Db 2197 AATGCTCGGTTTGTCTTATGCGCATACCGACATAAATGACCAAAAGTACACTGGCTAT 2256
Qy 2384 CCTACTGTTTAAAGAACTCGGGGAATGATGTTTCGTTTGTAGAAATTCGGTGGAGAGCT 2443
Db 2257 TCTCTCTTAAAGGAAGCTGGGAAATGATGCTTCTGGTATGAAATGTGAGAGGACTATC 2316
Qy 2444 CCGA-----TTTGCTTAGATGAAGTGTCTATTTGAGCAGTACATGCCCTTCATGAATG 2500
Db 2317 CCGTAGTTGCTTCAGAGCTCGGCTTTGGTGGATACCCACACGCCATTTCTAAACCTTA 2376
Qy 2501 CAGTTTCTATGACATCAGGAGGTTTAAAGAACAGGGAACAGAAAGCTCGTGAATTT 2560
Db 2377 GAGATGATCTATGACATCAGAAATGACTTTAAGMAAACGGCACAGAGSCGTTCTTTC 2436
Qy 2561 GGAAGTAGCGCTTTGTGAATCTTGCTTACCTTACCTATCGGATCCGATTTGATAGGAATCA 2620
Db 2437 CAAAGTGAAGACCTCTTCAATCTAGCGGTTCTCTGAGGATAAATTTGAGAA-----A 2490
Qy 2621 GACTGCCAAGATGCAAGTCAATCTAATCTTGTGTTATACTGTGATCTTGTTCGTAGT 2680
Db 2491 TTCTCCGATAGTCTAGATGATCTCTCCATAGCTTACGTTCCCGATGTGATTCGTAAT 2550
Qy 2681 AACCCGAGCTGTACGACAACTCGGAATAGCGGTGATTTCTTGGAAACCTTCGGTAGC 2740
Db 2551 GATCCAGCTCAGCAGCAACTCTTATGGTTCTTGGGGAATTTCTGGTGCACATGTGTACA 2610
Qy 2741 AATTGGCAAGACAAGCTTTAGTCTCTGTCAGGGAACCAATTTTGTCTTAACTCAAT 2800
Db 2611 AGTTTGTACAGAAAGTCTTCTTGTAGTGTGGAATCATCATGCTTGTCTTCAAC 2670
Qy 2801 TTTGAAGCTTTAGCCAAATTTCTTTTGAATTCGTTGGGTGCTCATCTCGCAATTAAGTGA 2860
Db 2671 TTTGAAGTTTTCAGTCAAGTTTGAAGTCAGTTCGAGGTTCTTCTCGTAGCTATGCTATC 2730
Qy 2861 GACTTAGAGCAAAATACCAATTTCTAA 2887
Db 2731 GATCTTGGAGGAAGATTTCGATTTTAA 2757

XX AAA30851;
 XX AC
 XX DT 29-AUG-2000 (first entry)
 XX Chlamydia antigen CPN100638 full length coding sequence.
 DE
 DE Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
 KW therapy; upper respiratory tract disease; bronchitis; sinusitis;
 KW asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma;
 KW ds.
 XX OS Chlamydia pneumoniae.
 XX
 XX Key Location/Qualifiers
 FH 101.2887
 FT CDS
 FT /*tag= a
 FT /product= Chlamydia antigen CPN100638
 FT
 PN WO200032794-A2.
 XX
 XX 08-JUN-2000.
 XX
 XX 01-DEC-1999; 99WO-CA01147.
 XX
 XX 01-DEC-1998; 98US-0110339.
 PR 01-DEC-1998; 98US-0110340.
 PR 01-DEC-1998; 98US-0110427.
 PR 01-DEC-1998; 98US-0110428.
 PR 01-DEC-1998; 98US-0110438.
 XX
 XX (CONN-) CONNAUGHT LAB LTD.
 PA
 XX
 XX Murdin AD, Oomen RP, Wang J;
 PI
 XX
 XX WPI: 2000-412339/35.
 DR P-PSDB; AAY90239.
 XX
 XX Nucleic acids encoding polypeptide antigens from Chlamydia useful for
 FT preventing, diagnosing and treating diseases such as community acquired
 PT pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
 PT asthma -
 XX
 XX Claim 2; Fig 5; 174pp; English.
 XX
 XX This sequence encodes a Chlamydia antigen of the invention, designated
 CC CPN100638. The nucleic acids (and their complementary sequences) may be
 CC used as diagnostic agents for detecting the presence of nucleic acids
 CC encoding Chlamydia antigens in samples according to standard methods,
 CC and therefore, for diagnosing Chlamydia infections. For example, they may
 CC be used as primers and probes for diagnostic polymerase chain reaction
 CC (PCR) assays. Antisense sequences may be used to down regulate
 CC expression of the proteins and may be used to treat infections. The
 CC nucleic acids may also be used to produce the protein antigens they
 CC encode according to standard recombinant DNA methodologies. The
 CC proteins may then be used as antigens for the production of antibodies
 CC (i.e. as vaccines) for preventing infection by Chlamydia. The
 CC antibodies may also be used as diagnostic reagents for detecting
 CC infections. Chlamydia is a pathogen implicated in the development of
 CC (for example) community acquired pneumonia, upper respiratory tract
 CC disease (especially bronchitis and sinusitis, asthmatic bronchitis,
 CC adult-onset asthma and acute exacerbations of asthma in adults.
 XX
 XX Sequence 2950 BP; 855 A; 724 C; 562 G; 809 T; 0 other;
 SQ
 Query Match 17.3%; Score 518.2; DB 21; Length 2950;
 Best Local Similarity 53.3%; Pred. No. 3.4e-133;
 Matches 1427; Conservative 0; Mismatches 1173; Indels 75; Gaps 13;
 QY 243 AGATGCTGGAACTACCTACCTATTATTAAGGGAAATGTCACCTAGAAAATATTCCTGGAA 302
 DB 258 ATGCAGATGGAATCTATATCTACACAGGGAGTGTCTC---AATCACCATGCGGAT 314

QY 303 CAGGCACAGCAATCACAAAAGCTGTTTTTAACAACACATAAGGGCGATTTGACTTTTCACAG 362
 DB 315 CTCGACAGCTTAACCGCTTCTGCTTTTAAAGAACTACTGGGAATCTTTCTTTCCAAAG 374
 QY 363 GTAAACGGAACTCTCTATTGTTCCAAACGGTGGATGACGGGACTCTAGCAGGGGCTGCTG 422
 DB 375 GCCACGGCTACCAATTTCTCTACAAAATATCGATCGGG-----AGCGAACTGTACCT 428
 QY 423 TTAACAGCAGCTGTGTAGATAAATCTACACGTTTATAGGGTTTCTTCGCTATCTTTTA 482
 DB 429 TTACCAATCAGCTGCAATAAAGCTTCTCTCTTTTCAGGATCTCTCTATTGTCACATAA 488
 QY 483 TTGCGTCTCTCTGGAAGTTTCGATAAATACCGGCAAAAGAGCCGCTTAGCTGCTCTACGGTA 542
 DB 489 TACAAACACCAAGATGCT-----ACCACAGGAACAGGAGCCATCAAGTCCACAGAGCTT 542
 QY 543 GCTTGAGTTTGAACAATAATGTAGTTTCTCTCTCAGCAAAAATCTTCAACGGTAATG 602
 DB 543 GTTCTATTCAAGTCGAACATAT---AGTTGCTACTTTTGGCCAAAATCTTTCTATGACAAATG 599
 QY 603 GCGGTGCTATCACCGCAAAAAGCTCTTTTCAATAACAGGGACTACAATGTACGCTCTGTTTT 662
 DB 600 GAGCGGCTCTCCAGGAGCTCTATCAGTCTATCGCTAAACCCCAACCTAAC---GTTTG 656
 QY 663 CTGAAAATACCTCTCAAAAGAAAGCGGAGCCATTACAGCTTCCGATGCCCTTACCAATTA 722
 DB 657 CCAAAAACAAAGCAACGCAAAAAGGGGTGCCCTCTATTCCACGGGAGGATTACAAATTA 716
 QY 723 CTGGAACCAAGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGATTTCTGGAGCTGCA 782
 DB 717 ACATAGCTTAACTCAGCATCATTTTCTGAAAATACCGCGCGCAACAAATGCGGAGCA 776
 QY 783 TTTTACAGAAGCTCGTGACTATTCTTAATAATGCTAAAGTTTCTTTTATTTGCAATA 842
 DB 777 TTTACACGGAAGCTAGCAGTTTTTATTAGCAGCAACAAGCAATAGCTTTATAAACAATA 836
 QY 843 AGGTACAGAGCGAGCTCTCTCAACAGGGGGATATGTCAGAGGTGCTATCTGTGCTT 902
 DB 837 GTGTGACCG-----CAACCTCAGCTACAGGGGAGGCCATTACTCTAGTA 881
 QY 903 ATAAAACTAGTACAGATATAAGGTCAACCTCAGCTGGAATCAGATGTACTCTTCAGCA 962
 DB 882 GTACATCAGCCCCCAACACAGTCTTAACTCTATCAGCAACGCGGAACGTGAATTTATAG 941
 QY 963 ACATACATCGACAACAGCGGAGGAGCTATCTATGTGAAAAGCTCGAAGCTGGCTCG 1022
 DB 942 GAAATACAGCAATTAAGTGTGGGGGCAATTTATCTGACAATCTAGTTCTTTCTTCTG 1001
 QY 1023 GAGGACTTACCTTATTTCAGTAGAATAATGTCATGAGGTACAGCTCTCTAAAGGTGGAG 1082
 DB 1002 GAGGACTAGCTTTTAAACAACTCTGGCTATGATCTGCACTCTCTTAGGAGGAG 1061
 QY 1083 CCATAGCTATCGAAGATAGTGGGAATGAGTTTATCCGCGATAGTGGTGAATGTCT 1142
 DB 1062 CAATTGCGATGCTGACTCTGGATCTTTGAGTCTTTTGGCTCTTGGTGGAGACATCACTT 1121
 QY 1143 TTTTAGGGAATACAGT-----CACTTCTACTCTCTGGGCAATAGAACTAGTA 1193
 DB 1122 TTGAAGGAACACAGTAGTCAAGAGGAGCTTCTTCGAGTCAGACCCTACCGAAAATCTTA 1181
 QY 1194 TCGACTTAGGA---ACGAGTGCAAAAGATGACAGCTTTGCGTTCTGCTGCTAGAGCCA 1250
 DB 1182 TTAACATCGAAAACACCAATGCTAGATTTGTACAGCTGCGAGCTCTCAAGGCATACTA 1241
 QY 1251 TCTACTTCTATGATCCATACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAG 1310
 DB 1242 TCTACTTCTATGATCTCTATACAACTAGCATCACTGCAGCTCTCTCAGATGCTCTAAACT 1301
 QY 1311 TTAATGAGACTCCGGCAGATTTCTGCACTACAATATACAGGGAACATCATCTTTACAGAG 1370
 DB 1302 TAAATGGTCTGACCTTGCAGGAATCTCGCATATCAAGGAACCATGCTATTTCTGGAG 1361
 QY 1371 AAAAGTTATCAGAGACAGAGGCGCGCAGATTTCTTAAATACTTACTTCGAAAGCTTACTACAGC 1430

Db 1362 AGNAGCTTCGAGAGAGAGCTGAGAGCTGATATCTCAATCTCAATTCAGCAAC 1421
Qy 1431 CTGTAACTCTTTCAGAGGTACTCTATCTTTTAAACATGAGTGAATCTGAGACTCAGG 1490
Db 1422 CTCTAACTCTTGGGGAGGCAACTCTCTTTAAATCAGAGTCACTCTAGTGTCTAAGT 1481
Qy 1491 CATTCACCTCAACAGGAGATTCCTGCTCGAATGAGCTAGGAATCTCTAGAACCTG 1550
Db 1482 CTTTTGGCAATCTCGGGCTCTACCTCTCATGATGTCAGGGCCACATTAGAAACG 1541
Qy 1551 CTGATCTAGCACATAAACAATTTGGTCAATTAACATCAGTCTCTATAGAGGTGCAAGA 1610
Db 1542 CTGATGGGATCACTATCAATAATCTTGTCTCAATGTAGATTCCTTAAAGAGAGCAAGA 1601
Qy 1611 AGGCAAAATAGAAACCAAGCTACGTCAAAAATCTGATTTATCTGGAAACCATCACTT 1670
Db 1602 AGGCAAGCTTAAAGCAACAACAAGCAAGTCAAGACGTCACTTTATCTGGATCGCTCTC 1661
Qy 1671 TATTGGACCCGAGCGGACCGTTTATGAAATCATAGTTTAAAGAAATCCTCAGTCTCAG 1730
Db 1662 TTGTAGATCTTCTGGAAATGCTACGAAGATGCTCTTGGAAATACCTCAAGTCTTTT 1721
Qy 1731 ACATCTAGAGCTCAAAAGCTT-----CTGGAATCTTAACAGCACCGCAGTGCAG 1784
Db 1722 CTGTCTCACTCTACTGTCTGACGACCCCGCAATATTCACATCAAGACTAGTCTGCTG 1781
Qy 1785 ATCCTTAATGGGTGAGAAATTCATTAACGCTATCAGGGAATCTGGGCCCAATTTGTT 1844
Db 1782 ATCCCTAGAAATAATCTTATCCATTTGGGATACCAAGGAATTTGGCATTTCTTGGC 1841
Qy 1845 GGGGACAGGGG-----TTTACGACTGCAACCTTCAACTGGACTAAACCTGGCTATA 1898
Db 1842 AAGAGGATCTGGGACTTAAATCCAAAGCAGCACTCTTACCTGGACAAAACAGGATACA 1901
Qy 1899 TTCTTAATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAG 1958
Db 1902 ATCGAATCTGAGCTGCTGGACCTTAGTTGCTAACCGCTATGGGATCTTTGTTG 1961
Qy 1959 ATATTAGCTCTCTCAATATCTTATGGAGACTGCAAAACGAGGGTTGCGGGAGACCGTG 2018
Db 1962 ATGTGCGCTCCATACACAGCTGTAGCCACTAAAGTACGCCAATCTCAAGAAACTCGCG 2021
Qy 2019 CTTTTGGTGTGCTGATTAATCTTCACTTCCATAGGATAGTACAAAACAGCAGCGG 2078
Db 2022 GCATCTGGTGAAGGATCTCGAACTCTTCCATAAAGATAGCAGAGATAAATAAG 2081
Qy 2079 GGTTTCGCCATTTGAGTGGGGTTATCTCATAGAGGAACCTACATACCTTGTTCAGATA 2138
Db 2082 GTTTTCGCCACATAAGTGCAGGTTATCTGTAGAGCGACTACACATTAGCTTCTGATA 2141
Qy 2139 AGATCTTAGTGTGCAATTTTGTGAGCTCTTTGGAGAGATAGACTACTTTGTAGCTA 2198
Db 2142 ATCTTATCACTGACGCTCTCGCCAAATTTTCGGGAAAGATAGAGATCACTTTTAAATA 2201
Qy 2199 AGAATCAAGGTACAGTCTACGAGGAATCTCTATTTACAGCAACAACCACTATATCT 2258
Db 2202 AAAATAGGCTTCTGCTATGACGCTCTCTCCATCTCCAGCATCTAGCAGCTTCTCTT 2261
Qy 2259 CTCCTTCCTGCAACTACGCGCTTGTGTTGCTTAATGTTCTCATAGAGATTCCTGTTC 2318
Db 2262 CTCCAAGCTTGTATC-----GCTACCTTCTGGATCTGAAAGTGAAGCAGCTGTCC 2312
Qy 2319 TCTTTTCAGGAACCTTAGCTACACCATACGGATACGATCTGAAACCAAGTATACAA 2378
Db 2313 TCTTTGATGCTCAGATCAGCTTATCTATAGTAAATACTATGAAACCTATTACACCC 2372
Qy 2379 CATATCTCTACTGTTAAAGAGAGCTGGGGAATGATGTTTCGCTTTAGAAATTCG---GTG 2435
Db 2373 AAGCAACCAAGAGAGAGCTCGTGGTATATGACGCTTTCGCTCTGGAACCTTGCAGCT 2432
Qy 2436 GAAGAGCTCCGATTTGCTTAGATGAAGAGTGTCTTATTTGAGCAGTACATGCCCTTATGA 2495

Db 2433 CCCTACCACACACTGCTTTTAAGCCATGAGGGTCTCTTCCACGGGTATTTTCTTTTCATCA 2492
Qy 2496 AATTGCAAGTTTGTATGACATCAGAGAGGTTTAAAGAAC---AGGGAACAGAGCTC 2552
Db 2493 AAGTAGAAGCTTCGTACATACCAAGATAGCTTCAAGAAACGTAATACCTTGGTAC 2552
Qy 2553 GTGAATTTGGAAGTAGCCGCTTTGTGAATCTTCCCTTACCTATCCGGATCCGATTTGATA 2612
Db 2553 GATCTTTCGATAGCGGTGAATTAATTAACGTCCTGTGCTATTGGAATTAACCTTCGAGA 2612
Qy 2613 AGGATCAGACTGCCAAGATGCAACGTACATCTAATCTTGTGTATATGTTGATCTTG 2672
Db 2613 GATTCTCGAARACAGCGTGCCTTTACGAAGTACTGTCACTACGTTCGCGATGTCT 2672
Qy 2673 TTCTAGTAACCCGCACTGTACGACCAACCTGCGAATTTAGCGGTGATTTTGGAAACCT 2732
Db 2673 ATCTAGAATCTGACTGCAACGACGCTCTCTAATCAACAATACCTCGTGGAAACTA 2732
Qy 2733 TCGGTAGAAATTTGGGCAAGCAAGCTTTAGTCTTCTGTCGAGGGAACCAATTTTGTCTTA 2792
Db 2733 CAGGAACGAATCTCTCAAGCAAGCTGATCGAAGAGCAGGGATCTTTTATGCCCTCT 2792
Qy 2793 ACTCAATTTTGAAGCCTTTAGCCAAATTTTCTTTTGAATTTGCGTGGTCACTCGCAAT 2852
Db 2793 CTCCAAATCTTGGTCAAGTAACCTATCTATGAAATTCGTGATCTTCAAGCAGCT 2852
Qy 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTAA 2887
Db 2853 ACAATGCAGATCTGGAGGTAAGTTCAGCTTCTAA 2887

RESULT 15
ABL91200
ID ABL91200 standard; DNA; 2787 BP.
XX
AC ABL91200;
XX
DT 29-JUL-2002 (first entry)
XX
DE Chlamydia pneumoniae cp6731 ORF DNA, SEQ ID NO:34.
XX
KW Chlamydia pneumoniae cp6731 ORF DNA, SEQ ID NO:34.
KW human respiratory disease; antigen; immunogen; vaccine; diagnosis;
KW coronary artery disease; cardiovascular disease; atherosclerosis;
KW cerebrovascular disease; carotid artery stenosis; myocardial infarction;
KW strain CWL029; open reading frame; ORF; gene; ds.
XX
OS Chlamydia pneumoniae.
XX
PH Key Location/Qualifiers
CDS 1..2787
FT /*tag= a
FT /product= "cp6731"
FT sig_peptide 1..78
FT mat_peptide 79..2784
FT /*tag= b
FT /*tag= c
FT /product= "Mature protein"
XX
PN WO200202606-A2.
XX
PD 10-JAN-2002.
XX
PF 03-JUL-2001; 2001WO-IB01445.
XX
PR 03-JUL-2000; 2000GB-0016363.
PR 11-JUL-2000; 2000GB-0017047.
PR 21-JUL-2000; 2000GB-0017983.
PR 07-AUG-2000; 2000GB-0019368.
PR 18-AUG-2000; 2000GB-0020440.
PR 14-SEP-2000; 2000GB-0022583.
PR 10-NOV-2000; 2000GB-0027549.
PR 22-DEC-2000; 2000GB-0031706.

XX (CHIR-) CHIRON SPA.
 XX PA
 XX PI
 XX Ratti G, Grandi G;
 XX WPI; 2002-154726/20.
 DR N-PSB; ABB90542.
 XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes -
 XX Claim 5; Page 57-58; 364pp; English.
 XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is
 CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
 CC the invention.
 XX SQ Sequence 2787 BP; 814 A; 689 C; 535 G; 749 T; 0 other;
 Query Match 17.2%; Score 516.6; DB 24; Length 2787;
 Best Local Similarity 53.3%; Pred. No. 9.2e-133;
 Matches 1426; Conservative 0; Mismatches 1174; Indels 75; Gaps 13;
 QY 243 AAGATCTCGAAGTACCTATTTAAGGGAATGTCTACTAGAAATATTCGGA 302
 DB 158 ATGCAGATGGAATCTATTAATCTAACAGGGGATGTCTC---AATCCCAATGCGGAT 214
 QY 303 CAGGCACAGCAATCAAAAAGCTGTTTAAACAACACTAAGGGCGATTTGACTTTTCACAG 362
 DB 215 CTCGACAGCTCTAACCGCTTCTGCTTTAAGAAACTACTGGGAATCTTCTTTCCAG 274
 QY 363 GTAAACGGGAATCTCTATTGTTTCCAAAACGGTGGATGACGGGACTGTAGCAGGGGCTGCT 422
 DB 275 GCCACGGCTACCAATTTCTCTCTACAAAATATCGATGCGGG-----AGCGAACTGTACCT 328
 QY 423 TTAACAGCAGCTGGTGGATTAATCTACCAAGTTTATAGGGTTTCTTCGCTATCTTTTA 482
 DB 329 TTACCAATACAGTGCATAATAGTTCTCTCTTTTCAGAAATCTCTTATTTGTCATTA 388
 QY 483 TTGCGTCTCTGGAGTTGCGATACTACCGGCAAAAGGAGCGGTAGTCTCTACGGGTA 542
 DB 389 TACAAACCCAGGAATGCT-----ACCACAGGAACAGGAGCCATCAAGTCCAAGGAGCTT 442
 QY 543 GCTTGGATTGCAAAAATGTCTGTTTCTTCAATTAACAGGGAATCAATGTCTGTTT 602
 DB 443 GTTCTATTGAGTGAACCTAT---AGTTGCTATTTTGGGCAAACTTTTCTAATGACAATG 499
 QY 603 GCGGTGCTATCACGCAAAAATCTTTCAATTAACAGGGAATCAATGTCTGTTT 662
 DB 500 GAGGCGCTTCCAGGCGAGCTCTATCAGTCTATGCTTAACCCCAACCTAAC---GTTTG 556
 QY 663 CTGAAAATACCTCTCTCAAGAGGCGGAGCGCAATTCAGACTTCCGATGCCCTTACATTA 722
 DB 557 CCAAAACCAAGCAACGCAAAAAGGGGGTGCCTCTATTCCACGGGAGGATTAACAATTA 616
 QY 723 CTGGAACCAAGGGAGTCTCTTTTCTGCAAAATCTCTTCGATCTCGAGCTGCA 782
 DB 617 ACAATAGTTAACTCAGCATCATTTTCTGAAAATACCGCGGCAACAATGGCGGCA 676

QY 783 TTTTACAGAGCGCTCGGTGACTATTCTTAATAAAGTCTAAAGTCTCTTTTATTGCAATA 842
 DB 677 TTTACAGGAGCTAGCAGTCTTTTATAGCAGCAACAAGCAATTAGCTTTTATAACAATA 736
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(without alignments)
7929.038 Million cell updates/sec

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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 11139956

Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
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Db 34657 C 34657

RESULT 2

US-09-198-452A-1/c

; Sequence 1, Application US/09198452A

; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
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Query Match 17.0%; Score 509.8; DB 4; Length 1230025;
 Best Local Similarity 52.7%; Pred. No. 2.7e-137;
 Matches 1410; Conservative 0; Mismatches 1184; Indels 81; Gaps 11;

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|----|--------|---|--------|
| QY | 247 | TGCTGGAACCTACCTACCTATTTAAGGGAATGCTACTAGAAAATATTCCTCGAACAGG | 306 |
| Db | 518045 | TACTGGAATAGACTATCTCTGACAGAGATATACTCTGCAAAACCTTGGGATTCGG | 517987 |
| QY | 307 | CACAGCAATCACAAGAGCTGTTTAAACAACATAAGGCGGATTTGACCTTTCACAGTAA | 366 |
| Db | 517986 | --CAGCTTTAACGAAGGTTGTTTTCTGACACTACGGATCTTTAAGCTTTGCCGGTAA | 517929 |
| QY | 367 | CGGGAATCTCTATTGTTCCAAACGGTGGATGAGGAGCTGTAGCAGGGGCTGCTGTAA | 426 |
| Db | 517928 | GGGGTACTCATTCTCTTTTAAATATNAAGTCTAGTGTGAAGGCGCANACTTCTGTT | 517869 |
| QY | 427 | CACGACGGTGGTAGATAAATCTACCAAGTTTATAGGGTTTCTTCGCTATCTTTTATTGC | 486 |
| Db | 517868 | -----ACAACGTATAAAATCTGTCGCTAACAGGATTTTCGAGTCTTACTTTCTTAGC | 517816 |

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|----|--------|---|---------------|-----|
| QY | 487 | GTCTCTGGAAGTTCCGATTAACCTACCGGAAAGGAGCGGTAGCT---- | GCTCTACGGGTAG | 543 |
| Db | 517815 | GGCCCATCATCGGTAAATCACACCCCTCAGGAAAGGTGCAGTTAAATGTGGAGGGGA | 517756 | |
| QY | 544 | CTTGAGTTTGACAAAAAATGTCAGTTTGTCTTTCAGCAAAAATCTTTCAACGGATAATGG | 603 | |
| Db | 517755 | TCCTACATTTGATACAAATGGAACTAATTTATTTAAACAGATTAATCTGTGAGAAATGG | 517696 | |
| QY | 604 | CGGTGCTATCACCGCAAAAATCTTTCAITTAACAGGGACTACAATGTCAAGTCTGTGTTTC | 663 | |
| Db | 517695 | CGGACATTTCTACCAAGATCTTTCTTGAAAAACAGACGGGATCGATTTCTTTTGAAG | 517636 | |
| QY | 664 | TGAAATA-----CCTCCTCAAAAGAGGGAGCCATTCAGACTTCGATGCCCTTA | 716 | |
| Db | 517635 | GGAAATAATCGAGCGCAACAGGAAAAAGGTGGGCTATTTGTGCTACTGGTACTGTAG | 517576 | |
| QY | 717 | CCATTACTGGAACCAAGGGGAAGTCTCTTTTCTGACAATACTCTTCTCGGATTTGGAG | 776 | |
| Db | 517575 | ATATTACAAATAATACGGCTCTACCTCTTCTCGAACTAATTTGCTGAAGCTGCAGGTG | 517516 | |
| QY | 777 | CTGCAATTTTTCAGAAAGCTCGGTGACTAATTTCTTAATTAATGCTAAAGTTTCTTTATTG | 836 | |
| Db | 517515 | GAGCTATAAATAGCACAGGAAACTGTACAAATTACAGGGAATACGTCTCTTGATTTTCTG | 517456 | |
| QY | 837 | ACAAATAAGCTCACAGGAGCGAGTCTCTCAACACGGGGATATGTCAGGAGGTGCTATCT | 896 | |
| Db | 517455 | AAAAATGTGTGAC--AGCGACCGCAGGAAATGGAGGAGCTCTTCTCG----- | 517410 | |
| QY | 897 | GTGCTTATAAACTAGTACAGATATCTAAAGGTCAACCTCACTGGAATCAGATGTTACTCT | 956 | |
| Db | 517409 | -----AGATCCGATGTACCATACTCTGGGAATCAGATGTAACCTT | 517369 | |
| QY | 957 | TCAGCAAAATACATCGAACACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAAGTGG | 1016 | |
| Db | 517368 | TCTCAGGAACCAAGCTGTAGTCTAATGGCGGAGCCATTTATGCTAAGAAAGCTTACACTGG | 517309 | |
| QY | 1017 | CTTTCGGAGGA-----CTTACCCTATTTCAGTAGAAATAGTGTCAATCGAGGTACAGCT | 1069 | |
| Db | 517308 | CTTTCGGGGGGGGGGGTATCTCCCTTTCTTAACAATATAGTCCAAAGGTACCCTGCA | 517249 | |
| QY | 1070 | CCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATCAGTTTATCCGCCGATAGT | 1129 | |
| Db | 517248 | GGTAATGTTGGAGCCATTTCTATCTACTGCGAGCTGGAGAGTGTAGTCTTTCAGCAGAGCA | 517189 | |
| QY | 1130 | GGTGACATTTGCTTTTAGGGAATACAGTCACTTCTACTACTCC---TGGGACGAATAGA | 1186 | |
| Db | 517188 | GGGGACATTTACCTTCAATGGGAATGCCATTGTTGCAACTTACACCAAACTACGAAAAAGA | 517129 | |
| QY | 1187 | AGTAGTATCGACTTAGGAACGAGTGCAAGATAGTGGGGAATCAGTTTATCCGCCGATAG | 1246 | |
| Db | 517128 | AAATCTATTGACATAGGATCTACTGAAAGATCAAGAAATTACGTGCAATATCTGGGCAAT | 517069 | |
| QY | 1247 | GCCATCTACTTCTATGATCCCACTACAGGATCATCCACACAGTTACAGATGTCTTTA | 1306 | |
| Db | 517068 | AGCATCTTTTCTACGATCCGATTACTGCTAATAACGGCTGCGGATTTCTACAGATCTTTA | 517009 | |
| QY | 1307 | AAAGTTAATGACATCCGCGACATCTGCATACAAATATACAGGAAACATCATCTTTCACA | 1366 | |
| Db | 517008 | AAATCTCAATAGGCTGATCCAGGTAATAGTACAGATATATAGTGGGTGCGATTTCTTTCT | 516949 | |
| QY | 1367 | GGAGAAAAGTTATCAGACACAGAGCGCGCAGATTTCTPAAAAATCTTACTTCGAGGTACTA | 1426 | |
| Db | 516948 | GGTGAAGACTCTCTGAAGATGAGCAAAAGTTGACACAACTCATCTTACGCTGAAG | 516889 | |
| QY | 1427 | CAGCCTGTAACTTTTCAGGAGTACTCTATCTTTAAAAACATGAGTGAAGTCTGAGACT | 1486 | |
| Db | 516888 | CAGCCTGTAACTTAACTCAGGAAATTTAGTACTTAAACGTGGTGTCACTCTCGATAG | 516829 | |
| QY | 1487 | CAGGCAATTCACCAACAGGCAATTTCTCGTCTCGAAATGGAAGTGAAGAACTACTCTAGAA | 1546 | |
| Db | 516828 | AAAGGCTTTACTCAGACCGCGGGTTCCTCTGTTATTTATGATGCGGGCAACGTTAAAA | 516769 | |
| QY | 1547 | CC---TGCTGATACTAGCACCAATAAACAATTTGGTCAITTAACATCAGTCTTATAGACGGT | 1603 | |
| Db | 516768 | GCAAGTACAGAGGAGGTCACTTTTAAACAGGTCTTTCCATTTCTGTAGACTCTTTAGCGGAG | 516709 | |
| QY | 1604 | GCAAAAGAGGCAAAAATAGAACCAACCAAGCTAGCTCAAAAANAATCTGACTTTATCTCGAAC | 1663 | |
| Db | 516708 | GGTAAGAAAGTTGTAAATTTGTGCTTCTGAGCAAGTAANAATGTAGCCCTTAGTGGTCCG | 516649 | |
| QY | 1664 | ATCAGCTTTATTTGGACCCGACGGGCAAGTTTTATGAAAATCATAGTTTAAAGAAATCCTCAG | 1723 | |
| Db | 516648 | ATTCTTCTTTTGGATAAACCAAGGGAATCTTATGAAATCAGACTTAGGAAAAACTCAA | 516589 | |
| QY | 1724 | TCCTACGACATCTTAGAGCTCAAAGCTTCTGGAACTGTAAACAGCACCGAGTGACTCCA | 1783 | |
| Db | 516588 | GACTTTTTCATTTGTGCAGCTCTCTGCTCTGGGTACTGCAACAACACTACAGATGTTCCAGCG | 516529 | |
| QY | 1784 | GATCCTATAATGGGTGAGAAATTCATTACGGCTATCAGGGAACCTTGGGGCCCAATTGTT | 1843 | |
| Db | 516528 | GTTCCTACAGTAGCAACTCCTCAGGCACTATGGGTATCAAGGTACTTTGGGGAATGACTTGG | 516469 | |
| QY | 1844 | TGGG-----GACAGGGGGCTTCTACGACTGCAACTTCAACTGGACTAAAACT | 1891 | |
| Db | 516468 | GTGATGATACCGCAAGCACTCCAAAGACTTAAGACAGCGACATTAGCTTTGGACCAATAGC | 516409 | |
| QY | 1892 | GGCTATATTCCTAATCCGAGGGTATCGGCTCTTTTAGTCCCTAATAGCTTATGGAATGCA | 1951 | |
| Db | 516408 | GGCTACCTTCCGAATCTCTGAGCGTCAAGGACCTTTAGTTCCTAATAGCTTTGGGGATCT | 516349 | |
| QY | 1952 | TTTATAGATATTAGCTCTCTCCATTTATGAGAGCTGCAACGAAAGGGTTGCAGGA | 2011 | |
| Db | 516348 | TTTTCAGACATCCCAAGCCATTCAGGTCTCATAGAGAGAGTCTTTGACTCTTTGTTCA | 516289 | |
| QY | 2012 | GACGTGCTTTTGGTGTGTGGATATCTAACTTCTTCCATAAGGATAGTACAAAAACA | 2071 | |
| Db | 516288 | GATCAGGCTTCTGGGCTGCGGAGTCGCCAATTTCTTAGATAAGATAAGAAAGGGAA | 516229 | |
| QY | 2072 | CGACGCGGTTTCCGCAATTTGAGTGGCGTTATGTCATAGGAGGAACTCATACTTTGT | 2131 | |
| Db | 516228 | AAACCAAAATCCGTCATAAATCTGGTGGATATGCTATCGGAGGTGACGCGCAACTTGT | 516169 | |
| QY | 2132 | TCAGATAAGATCTTAGTGTGCAATTTTGTCAAGCTCTTTTGAAGAGATAGAGACTTCTT | 2191 | |
| Db | 516168 | TCTGAAAACCTTAAATAGCTTTGCTTTTGCCTTTTGCCTTTTGCCTTTTGAAGATTTCTTA | 516109 | |
| QY | 2192 | GTAGCTAAGATCAAGGTACAGTCTACGAGGAACTCTCTATTTACCAGCAACAGAAACC | 2251 | |
| Db | 516108 | GTGCTAAAAATCATACTGATACCTTATGACGAGGCTTCTATATCCAACACATTACAGAA | 516049 | |
| QY | 2252 | TATATCTCTCTTCTGCTTCAAACTACGGCTTTGTTGTTGTCTTATGTTCTCTACAGATT | 2311 | |
| Db | 516048 | TGTAGTGGGTTTCATAGTTGTCTTTAGATAAA---CTTCTGGCTCTTGGAGTCATAAA | 515992 | |
| QY | 2312 | CCTGTTCTCTTTTTCAGGAAACCTTTAGCTACCCCATACGATAACGATCTGAAAAACCAAG | 2371 | |
| Db | 515991 | CCCCTCGTTTTTAGAAGGCGCAGCTCGCTTATAGCCACGCTCACTAATGATCTGAAGACAAG | 515932 | |
| QY | 2372 | TATACACATATCTCTGTTTAAAGGAAGCTGGGGAATGATGTTTCGCTTTTGAATTC | 2431 | |
| Db | 515931 | TATCTGCTATCTCTGAGTGAAGGTTCTTTGGGGAATAATGCTTTTAAACATGATGTG | 515872 | |
| QY | 2432 | GGTGAAGAGCTCCGATTTGCTTAGATGAAGTGTCTTATTTGAGCAGTACATCCCTTC | 2491 | |
| Db | 515871 | GGAGTCTTCTCATTTCTTATCTCTGAATACCTGCAATTTGTTTATACCTATGCTCCATAC | 515812 | |
| QY | 2492 | ATGAAATTCAGTTTGTCTATGCACTCAGGAAGGTTTTTAAAGAACAGGGACAGAAGCT | 2551 | |
| Db | 515811 | ATCAAACTGAATCTGACCTATACGTCAGGACAGCTTCTCGGAGAAAGGTACAGAGGA | 515752 | |
| QY | 2552 | CGTGAATTTGGAAGTAGCCGCTCTGTGAATCTTCCCTTACCTATCGGATCCGATTTGAT | 2611 | |
| Db | 515751 | AGATCTTTTGTATGACAGCAACTCTTCAATTTATCTTTGCTATAGGGGTGAAGTTTGGAG | 515692 | |
| QY | 2612 | AAGGATCAGACTGCCAAGATGCAACGTACAACTCTTAACCTTTGTTTATCTGTGATCTT | 2671 | |

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Db 515691 AAGTTCTCTGATGTGAATGACTTTCTTTATGATCTGACTTTATCTATGTTCTGATCTT 515632
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QY 2852 TACAAATGTAGACTTAGGAGCAAAATACCAATTTCTA 2886
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RESULT 3
US-09-556-877-182
; Sequence 182, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
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US-09-556-877-182

Query Match 4.4%; Score 132.2; DB 4; Length 3021;
Best Local Similarity 48.8%; Pred. No. 2.6e-28; Indels 48; Gaps 5;
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QY 1836 CAATTTGTTGGGGACAGGGGCTTCTACGACTGCAACCTTCACTGGACTAAACTGGCT 1895
Db 2012 ATCTTAATACACAAATAATGGTCTTATCTACTCTGAAAGCTACATGGACTAAACTGGT 2071
QY 1896 ATATTCCTAATCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTTATGAATGCAATTA 1955
Db 2072 ATAACTCTGGGCTGAGCGAGTAGCTCTTTGGTTCCAAATAGTTATGGGATCCATTT 2131
QY 1956 TAGATATTAGCTCTCTCCATTAATCTTTAGGAGACTGCAAAAGAGGTTGAGGAGACC 2015
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QY 2016 GTGCTTTTGGTGTGCTGATTAATCTAACTTCTCCATAAGGATAGTACAAAACACGAC 2075
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QY 2076 GCGGGTTTCGCCATTTGAGTGGCGGTATGTGCATAGGAGGAAACCTACATACTTTGTCAG 2135
Db 2252 AGGATATCGGTATATAGTGGGGTTATCTCTTAGGAGCAACTCTTACTTTGATCA- 2310
QY 2136 ATAGATTTCTAGTCTGCAATTTGTACCTCTTTGGAGAGATAGACTACTTTGTAG 2195

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Db 2311 --TCGATGTTGGTCTAGCATTTACGAAATTTTGGTAGATCTAAAGATTATGTAGTGT 2368
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Db 2406 TCTATCTACCAACAAAGCT-----TTATGTGGATCCTATTGTTGCGAGATCGCTT 2456
QY 2316 TTTCTTTTTCAGAAAACCTTAGCTACACCCATACCGGATAACGATCTGAAAACCAAGTATA 2375
Db 2457 TATCCGT-----GCTAGCTACGGGTTTGGAAATCAGCATATGAAAACCTCATATA 2506
QY 2376 CAACATATCCTACTGTTTAAAGAAAGCTGGGGAATGATAGTTTCGTTTGAATTCGATG 2435
Db 2507 CATTTGCGAGAGGAGAGCGATGTTCTTGGGATAATAACTGTCTGCTGGCGAGAGATTGGAG 2566
QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAAGTCTCTATTTTGGCAGGTACATG--CCCTTCA 2492
Db 2567 CGGGATTACCGATTGTGATTACTCCATCTAAGCTCTATTGAAATGAGTTGCGTCTTTTCG 2626
QY 2493 TGAATTTGCAGTTTGTCTATGCAATCAGGAGAGGTTTTAAAGAAACAGGAAACAGAGCTC 2552
Db 2627 TGAAGCTGAGTTTCTTATGCGGATCATGAATCTTTTACAGAGGAGAGCGATCAAGCTC 2686
QY 2553 GTGAATTTGGAAGTAGCGCTCTTGTGAATCTTGCCTTACCTATCGGATCCGATTTGATA 2612
Db 2687 GGGCATTTCAAGAGCGGACATCTCTAAATCTATCAAGTTCTCTGTTGGAGTGAAGTTTGATC 2746
QY 2613 AGGAATCAGACTGCCAAGATGCAAGCTCAAACTTAACTCTTGGTTTATCTGTGGATCTTG 2672
Db 2747 GATGTTCTAGTACACATCTTAATAATATAGCTTTTATGGCGCTTATATCTGTATGCTT 2806
QY 2673 TTGCTAGTAACCCGAGCTGTACGACAACTGCGAATAGCGGTGATTTCTTGAAAAAACC 2732
Db 2807 ATCGCACCATCTCTGCTACTGAGACAAACGCTCTATCCATCAAGAGACATGCAACACAG 2866
QY 2733 TCGGTACGAATTTGGCAAGACAGCTTTAGTCTCTTCTGTCAGGGACCATTTTTCCTTTA 2792
Db 2867 ATGCTTTTCATTTAGCAAGACATGAGTTGTTGGTTAGAGGATCTATGTATGCTTCTTAA 2926
QY 2793 ACTCAAAATTTGAAGCTTTTAGCCAAATTTTCTTTTGAATTTGCTGGGTGATCTCGCAAT 2852
Db 2927 CAGTATATAGAGTATATATGCCATGGAAGATATAGTATCAGATGCTCTTCTCGAGCT 2986
QY 2853 ACAATGACTTAGGAGCAAAATACCAATTTCTAA 2887
Db 2987 ATGTTTGTAGTGAGGAAGTAAAGTCCGGTTCTAA 3021

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RESULT 4

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US-09-620-412C-182
; Sequence 182, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-182

```

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Query Match 4.4%; Score 132.2; DB 4; Length 3021;
Best Local Similarity 48.8%; Pred. No. 2.6e-28; Indels 48; Gaps 5;
Matches 544; Conservative 0; Mismatches 523;

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QY 1776 TGACTCCAGATCCTATATGGGTGAGAAATCCATTCAGCGCTATCAGGAACTTGGGGCC 1835
Db 1952 TGACTCTAGGAATGAGATGCCCTAAGTAGGTATCAAGGAAGCTGGAAGCTTGGGTGGG 2011

QY 1836 CAATTGTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGCAATAAACTGGCT 1895
Db 2012 ATCCTAATACAGCAATATGTCCTTATACCTGGAAGCTACATGAACTAAACTGGGT 2071

QY 1896 ATATTCCTAATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTATGGAATGCAATTA 1955
Db 2072 ATAATCCTCGGCTGAGCGAGTAGTCTTCTGGTTCCTCAATAGTTTATGGGATCCATTT 2131

QY 1956 TAGATATTAGCTCTCTCCATTAATCTATGAGAGCTCAACCAAGGTTGCGAGGAGACC 2015
Db 2132 TAGATATACGATCTCGGCAATTCAGCAATTCAGCAAGTGTGATGAGGAGCTTGGGTGG 2071

QY 2016 GTGCTTTTGGGTGCTGGATTAATCACTTCTTCAAGGATAGTACAAAAACAGAC 2075
Db 2192 GAGGATTAAGGTTTCTGGAGTTTCAATTTCTTCTATCATGACCGGATGCTTAGGTC 2251

QY 2076 GCGGTTTCGCCATTTGAGTGGCGGTATGTCATAGGAGAACTTACATCTTGTTCAG 2135
Db 2252 AGGATATCGGTATATAGTGGGGTATTCCTTAGGAGCAAACTCCTACTTTGGATCA- 2310

QY 2136 ATAAGATTCTTAGTGTGCTGCAATTTGTACGCTCTTTGGAGAGATAGAGACTACTTTGTAG 2195
Db 2311 --TCGATGTTTGGTCTAGCAATTCAGGAGTATTTGGTAGTCTAAGGATTTAGTGT 2368

QY 2196 CTAGAATCAAGGTACAGTCTTACAGTACCGGCTTCTTATCCAGCAACCAAGGAGCT 2255
Db 2369 GTGCTTTTCAATCATGCTTGCATAGGATC-----CGTTTA 2405

QY 2256 TCTCTCTCTTCTGCAAACTACGCGCTTGTTCGTGCTTATGTTCTTACAGAGATTCCTG 2315
Db 2406 TCTATCTACCCCAACAGCT-----TTATGTTGATCTTATTTGTTGGAGATGCGTT 2456

QY 2316 TTCTCTTTTCAGGAAACCTTAGCTTACACCGATACCGATTCGAAACCAAGTATA 2375
Db 2457 TATCGGT-----GCTAGCTTACCGGTTTGGGAATCAGCATATGAACCTCATATA 2506

QY 2376 CAACATATCTTACTGTTAAAGGAAGCTGGGGAAATGATGTTTTCGCTTTAGAAATTCGGTG 2435
Db 2507 CATTTGCGAGAGAGAGCGATGTTGCTTGGGATAATAAATCTGCTGCTGAGAGATTGGAG 2566

QY 2436 GAAGAGCTCCGATTTGCTTAGTAGAAGTGTCTATTTGAGCAGTACATG-----CCCTCA 2492
Db 2567 CGGATTAACCGATTTGATTAATCCATCTAAGCTCTATTTGAATGAGTTGCGTCTTTTCG 2626

QY 2493 TGAATTTGCAAGTTGCTATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGAAAGCTC 2552
Db 2627 TGCAGCTGAGTTTCTTATGCGGATCATGATCTTTTACAGAGAGAGCGATCAAGCTC 2686

QY 2553 GTGAATTTGGAAGTAGCGCTTTGTGAATCTTTCCTTACCTACCGGATTCGGAATTTGATA 2612
Db 2687 GGGCATTTCAAGAGCGGACATCTCTAAATCTATCAGTTCTCTGAGTGAAGTTTGTATC 2746

QY 2613 AGGAATCAGACTGCCAAGATGCAAGTCAATCTTGGTTTATCTTGGTATCTGGAATCTTG 2672
Db 2747 GATGTTCTAGTACATCTCTAATAATATAGCTTTATGCGCGCTTATATCTGTGATGCTT 2806

QY 2673 TTCTGATGAACCCCGACTGTACGACAACTACGAAATTAGCGGTGATTTCTGGAAAACT 2732
Db 2807 ATCGCACCATCTCTGTTACTGAGACAACTGCTCTTATCCCATCAAGAGACATGGAACAG 2866

QY 2733 TCGGTACGAATTTGGCAGACAAAGCTTTAGTCCCTTCGTGAGGAAACCAATTTTCCTTTA 2792
Db 2867 ATGCTCTTTCATTTAGCAAGACATGAGTGTGGTTAGAGATCTATGATGCTTCTCTAA 2926

QY 2793 ACTCAAAATTTGAGCCCTTTAGCCAAATTTCTTTTGAATTTGGTGGGTCACTCCCAAT 2852
Db 2927 CAAGTAATATAGAGTATATGCCCCATGGAAGATATGAGTATCGAGATGCTTCTCGAGCT 2986
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QY 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTAA 2887
Db 2987 ATGGTTTGAGTGCAGGAAGTAAAGTCCGGTTCTAA 3021
```

RESULT 5

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US-09-598-419-182
; Sequence 182, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598.419
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-598-419-182
```

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Query Match 4.4%; Score 132.2; DB 4; Length 3021;
Best Local Similarity 48.8%; Pred. No. 2.6e-28;
Matches 544; Conservative 0; Mismatches 523; Indels 48; Gaps 5;
```

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QY 1776 TGACTCCAGATCCTATATGGGTGAGAAATCCATTCAGCGCTATCAGGAACTTGGGGCC 1835
Db 1952 TGACTCTAGGAATGAGATGCCCTAAGTAGGTATCAAGGAAGCTGGAAGCTTGGGTGGG 2011

QY 1836 CAATTGTTTGGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGAGTAAACTGGCT 1895
Db 2012 ATCCTAATACAGCAATTAATGCTCTTATACCTCTGAAAGCTACATGAGTAAACTGGGT 2071

QY 1896 ATATTCCTAATCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTA 1955
Db 2072 ATAATCCTCGGCTGAGCGAGTAGTCTTCTTTGGTTCCAAATAGTTTATGGGGATCCATTT 2131

QY 1956 TAGATATTAGCTCTCTCCATTAATCTTATGAGAGCTGCAACCAAGGTTGCGAGGAGACC 2015
Db 2132 TAGATATACGATCTCGGCAATTCAGCAATTCAGCAAGTGTGATGAGGAGCTTATTGTC 2191

QY 2016 GTGCTTTTGGGTGCTGGATTAATCACTTCTTCAATAGGATAGTACAAAAACAGAC 2075
Db 2192 GAGGATTAAGGTTTCTGGAGTTTCAATTTCTTCTATCATGACCGGATGCTTTAGGTC 2251

QY 2076 GCGGTTTCGCCATTTGAGTGGCGGTATGTCATAGGAGAACTTACATCTTGTTCAG 2135
Db 2252 AGGATATCGGTATATAGTGGGGTATTCCTTAGGAGCAAACTCCTACTTTGGATCA- 2310

QY 2136 ATAAGATTCTTAGTGTGCTGCAATTTGTGCTGAGCTTTTGAAGAGATAGAGACTACTTTGTAG 2195
Db 2311 --TCGATGTTTGGTCTAGCAATTTACCGAGTATTTGGTAGTCTAAGATTTAGTGT 2368

QY 2196 CTAGAATCAAGGTACAGTCTTACAGGAGAACTCTTATCCAGCAACCAAGGAGCTTATA 2255
Db 2369 GTGCTTTCAATCATGCTTGCATAGGATC-----CGTTTA 2405

QY 2256 TCTCTCTCTTCTGCAAACTACGCGCTTGTTCGTGCTTATGTTCTTACAGAGATTCCTG 2315
Db 2406 TCTATCTACCCCAACAGCT-----TTATGTTGATCTTATTTGTTGGAGATGCGTT 2456

QY 2316 TTCTCTTTTCAGGAAACCTTAGCTTACACCGATACCGATTCGAAACCAAGTATA 2375
Db 2457 TATCGGT-----GCTAGCTTACCGGTTTGGGAATCAGCATATGAACCTCATATA 2506

QY 2376 CAACATATCTTACTGTTAAAGGAAGCTGGGGAAATGATGTTTTCGCTTTAGAAATTCGGTG 2435
Db 2507 CATTTGCGAGAGAGAGCGATGTTGCTTGGGATAATAAATCTGCTGCTGAGAGATTGGAG 2566

QY 2436 GAAGAGCTCCGATTTGCTTAGTAGAAGTGTCTATTTGAGCAGTACATG-----CCCTCA 2492
Db 2567 CGGATTAACCGATTTGATTAATCCATCTAAGCTCTATTTGAATGAGTTGCGTCTTTTCG 2626

QY 2493 TGAATTTGCAAGTTGCTATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGAAAGCTC 2552
Db 2627 TGCAGCTGAGTTTCTTATGCGGATCATGATCTTTTACAGAGAGAGCGATCAAGCTC 2686

QY 2553 GTGAATTTGGAAGTAGCGCTTTGTGAATCTTTCCTTACCTACCGGATTCGGAATTTGATA 2612
Db 2687 GGGCATTTCAAGAGCGGACATCTCTAAATCTATCAGTTCTCTGAGTGAAGTTTGTATC 2746

QY 2613 AGGAATCAGACTGCCAAGATGCAAGTCAATCTTGGTTTATCTTGGTATCTGGAATCTTG 2672
Db 2747 GATGTTCTAGTACATCTCTAATAATATAGCTTTATGCGCGCTTATATCTGTGATGCTT 2806

QY 2673 TTCTGATGAACCCCGACTGTACGACAACTACGAAATTAGCGGTGATTTCTGGAAAACT 2732
Db 2807 ATCGCACCATCTCTGTTACTGAGACAACTGCTCTTATCCCATCAAGAGACATGGAACAG 2866

QY 2733 TCGGTACGAATTTGGCAGACAAAGCTTTAGTCCCTTCGTGAGGAAACCAATTTTCCTTTA 2792
Db 2867 ATGCTCTTTCATTTAGCAAGACATGAGTGTGGTTAGAGATCTATGATGCTTCTCTAA 2926

QY 2793 ACTCAAAATTTGAGCCCTTTAGCCAAATTTCTTTTGAATTTGGTGGGTCACTCCCAAT 2852
Db 2927 CAAGTAATATAGAGTATATGCCCCATGGAAGATATGAGTATCGAGATGCTTCTCGAGCT 2986
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| | | | |
|----|------|---|------|
| Qy | 2436 | GAACAGCTCCGATTTGCTTAGATGAAGTGTCTATTGTGACGATCAATG---CCCTTCA | 2492 |
| Db | 2567 | CGGGAATTACCGATTGTGATTACTCCATCTAGCTCTATTTGAATGAGTGTGGTCTCTTCG | 2626 |
| Qy | 2493 | TGAAATTTGCAGTTTGTCTATGCAATCAGGAAGGTTTTAAAGACACGGACAGAGCTC | 2552 |
| Db | 2627 | TGCAAGCTGAGTTTCTTTATGCCGATCATGATCTTTTACAGGAAGCGATCAAGCTC | 2686 |
| Qy | 2553 | GTGAATTTGGAAGTAGCGGCTTTGTGAATCTTGTGCTTACCTATCGGGATCCGATTTTGATA | 2612 |
| Db | 2687 | GGGCAATTCAGAGCGGACATCTCCTAAATCTATCAGTTCCTGTGGAGTGAAGTTTGATC | 2746 |
| Qy | 2613 | AGGAATCAGACTGCCAAGATGCACAGTCAGTAACTAACTCTTGGTTATCTGTGGATCTTG | 2672 |
| Db | 2747 | GATGTTCTTAGTACATCCTCAATAAATATAGCTTTATGGCGGCTTATATCTGTGATGCTT | 2806 |
| Qy | 2673 | TTCGTAGTAACCCGACTGTACGACACACTCGCAATTAGCGGTGATTTCTTGAAACCT | 2732 |
| Db | 2807 | ATCGCACCATCTCTGGTACTGAGACAAAGCTCCTATCCCATCAAGACATGACACACAG | 2866 |
| Qy | 2733 | TCGGTACGAATTTGGCAAGACAAGCTTTAGTCTCTGTGACGGGAACCATTTTTCGTTTA | 2792 |
| Db | 2867 | ATGCTTTTCATTTTAGCAAGACATGGAGTTGTGGTTAGAGGATCTATGATGCTTCTCTAA | 2926 |
| Qy | 2793 | ACTCAAAATTTGAAGCCCTTTAGCCAAATTTCTTTTGAATTTGCGTGGGTCTATCTCGCAATT | 2852 |
| Db | 2927 | CAAGTAATATAGAAGTATATGGCCATCGCAATATAGTATCGAGATGCTTTCGAGGCT | 2986 |
| Qy | 2853 | ACAAATGTAGACTTAGGACGAAAAATACAAATTCATA | 2887 |
| Db | 2987 | ATGCTTTTGAAGTCAGGAAGTAAGTCCCGTTCTTAA | 3021 |

RESULT 6

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US-09-556-877-170
; Sequence 170, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-170

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|----|------|--|--|------|
| Db | 2060 | | TAGATATACGATCTGCGCAITTCAGCAATTCAGCAAGTGTGATGGCGCTTATTGTC | 2119 |
| Qy | 2016 | | GTGCTTTTGGTGTGCTGGATATCTAACTTTCCATAAGTAGTACAAAACACGAC | 2075 |
| Db | 2120 | | GAGGATATGGGTTTCTGGAGTTTCGAATTTCTTATCATGACCGGATGCTTAGGTC | 2179 |
| Qy | 2076 | | GCGGTTTCGCAATTCAGTGGCGGTATCTCATAGGAGAAACCTACATCTGTTCAG | 2135 |
| Db | 2180 | | AGGATATCGTATATTAGTGGGGTTATTCCTTTAGGAGCAAACTCCTACTTTGGATCA | 2238 |
| Qy | 2136 | | ATAAGATTCTTAGTGCTGCACTTTTGTGAGCTCTTTTGGAGAGATAGAGACTACTTTGTAG | 2195 |
| Db | 2239 | | TCGATGTTGGTCTAGCAATTCACCAAGTATTTGGTAGATCTAAAGATTATGTAGTGT | 2296 |
| Qy | 2196 | | CTAAGAAATCAAGGTACAGTCTACGGAGAACTCTCTATTACCAGCAACAGAAACCTATA | 2255 |
| Db | 2297 | | GTGCTTCCAAATCATGCTTGCATAGGATC-----CGTTTA | 2333 |
| Qy | 2256 | | TCCTCTTCCTTCGAAACTAGGCGCTTGTTGCTGTATGTTCTTACAGAGATTCCTG | 2315 |
| Db | 2334 | | TCATCTACCCACAAGCT-----TTATGTGGATCCTATTGTTGGAGATCGGTT | 2384 |
| Qy | 2316 | | TTCTCTTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAACCAACTATA | 2375 |
| Db | 2385 | | TATCCGT-----GCTAGCTACGGTTTGGGAATCAGCAATAGAAACCTCATATA | 2434 |
| Qy | 2376 | | CAACATATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAAATCCGGT | 2435 |
| Db | 2435 | | CAATTGCAGAGGAGACGATGTTCGTTGGGATAATAACTGTCCTGGCTGGAGAGATTGGAG | 2494 |
| Qy | 2436 | | GAAGAGCTCCGATTTGCTTAGATAAAGTGCTCTATTGGAGCAGTACATG---CCCTTCA | 2492 |
| Db | 2495 | | CGGGAATPACCGATTGTGATTACTCCATCTAAGCTCTATTGTAATGAGTTGCGTCTTTCCG | 2554 |
| Qy | 2493 | | TGAAATTCGAGTTTGTCTATGCACATCAGGAGGTTTTAAAGAACAGGAGAAACAGAGCTC | 2552 |
| Db | 2555 | | TGCAGCTGAGTTTCTTATGCGCATCATGAATCTTTTACAGAGGAAGCGATCAAGCTC | 2614 |
| Qy | 2553 | | GTGAAATTGGAAGTAGCCGCTTTGTGAACTTTGCTCTTACTATCGGGATCCGATTTTGATA | 2612 |
| Db | 2615 | | GGGCAITTCAGAGCGGACATCTCTAAATCTATCAGTTCTCTGTTGGAGTGAAGTTTGATC | 2674 |
| Qy | 2613 | | AGGAATCAGACTGCCAAGATGCAACGTACAATCTAATCTTGGTTATCTGTGGATCTTG | 2672 |
| Db | 2675 | | GATGTTCTAGTACACATCCTAATAAATATAGCTTTATGGCGCTTATATCTGTGATGCTT | 2734 |
| Qy | 2673 | | TTCGTAGTACCCCGACTGTACGACAACTCGGAATTAGCCGTGATTTCTTGGAAACCT | 2732 |
| Db | 2735 | | ATCGCACCACTCTGTGATCTGAGACCAACGCTCCTATFCCCATCAAGAGACATGGACAACAG | 2794 |
| Qy | 2733 | | TCGGTACGAATTTGGCAAGACAGCTTTAGTCTCTTCGTGCGGGAACCAATTTTGCCTTA | 2792 |
| Db | 2795 | | ATGCCCTTCAATTAGCAAGCATGGAGTTGTGGTTAGAGGATCTATGATGCTTCTCTAA | 2854 |
| Qy | 2793 | | ACTCAAATTTGAAGCCTTTAGCCAAATTTCTTTTGAATTCGGTGGGTCAATCTCGCAATT | 2852 |
| Db | 2855 | | CAAGTAATATAGAAGTATATGCCATGGAAGATATCAGTATCGAGATGCTTCTCGAGCT | 2914 |
| Qy | 2853 | | ACAACTAGACTTAGGAGCAAAATACCAATTTCTAA | 2887 |
| Db | 2915 | | ATGGTTTGTGTCAGGAGTAAAGTCYGGTCTTAA | 2949 |

RESULT 7

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; RECDL /
US-09-620-412C-170
; Sequence 170, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C07

```



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; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-170

Query Match          4.4%; Score 131.4; DB 4; Length 2949;
Best Local Similarity 48.6%; Pred. No. 4.5e-28;
Matches 542; Conservative 2; Mismatches 523; Indels 48; Gaps 5;

QY 1776 TGACTCCAGATCCTATAATGGGTGAGAAATTCATTACGGCTATCAGGGAACCTTTGGGGCC 1835
Db 1880 TGACTCTAGGGAATGAGATGCCCTAAGTATGGCTATCAAGGAAGCTTGAAGCTTGGTGGG 1939
QY 1836 CAATTGTTGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAACCTGGCT 1895
Db 1940 ATCCTTAATACAGCAAAATATGGTCCCTTATFACCTCTGAAAGCTACATGGACTAAACCTGGCT 1999
QY 1896 ATATTCCTAATCCCGAGCGGTATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTTA 1955
Db 2000 ATAACTCTGGGCTGAGCGAGTAGCTCTTTGGTTCCAAATAGTTTATGGGATCCATTT 2059
QY 1956 TAGATATTAGCTCTCTCCATTATCTTATGGAGACTGCAAAACGAAGGGTTGCGAGGAGAC 2015
Db 2060 TAGATATACGATCGCGCATTCAGCAATTCAGCAAGTGTGGATGGCGCTCTTATTGTC 2119
QY 2016 GTCTTTTGGTGTGCTGAGTATCTAATCTTCTCCATAGGATAGTACAAAACAGCAG 2075
Db 2120 GAGGATATGGGTTCTCGAGTTTCGAAATTTCTCTATCATGACCGCATGCTTTAGGTC 2179
QY 2076 GCGGTTTCGCCATTTGAGTGGCGGTATGTCAVAGGAGAAACCTACATACCTTTGTCAG 2135
Db 2180 AGGGATATCGGTATATTATAGTGGGGTATTCTTCTAGGAGCAAACTCTCTTTGGATCA- 2238
QY 2136 ATAAGATTCTTAGTCTGCAATTTTGTGAGCTTTTGGAGAGATAGAGACTACTTTGAG 2195
Db 2239 --TCGATGTTTGGTCTAGCAATTTACCGAAGTATTGGTAGATCTAAAGATTATGTAGTGT 2296
QY 2196 CTAAGAATCAAGGTACAGTCTACGAGGAACTCTCTATTACCAGCAACAGCAACCTATA 2255
Db 2297 GTCGTTCCAAATCATCATCTTGCATAGGATC-----CGTTTA 2333
QY 2256 TCTCTCTTCTTCCAAACTACGGCTTGTGTTGTTCTTATGTTCTCAGAGATTCCTG 2315
Db 2334 TCTATCTACCAACAAGCT-----TTATGTGGATCCTATTGTTGGAGATCGGT 2384
QY 2316 TTCTCTTTTCAGGAACCTTAGCTACACCATACGGATAACGATCTGAAACCAAGTATA 2375
Db 2385 TATCCGT-----GCTAGCTACGGGTTGGGAATCAGCATATGAAACCTCATATA 2434
QY 2376 CAACATATCCTACTGTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAAATCGGTG 2435
Db 2435 CATTCGAGAGAGACGATGTTGCTTGGGAATAAATAACTGTCTGGCTGAGAGATTGGAG 2494
QY 2436 GAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTGAGCAGTACATG---CCCTTCA 2492
Db 2495 CGGGATTACCGATTGATTAATCTCCATCTAAGCTCTATTGATGAGTTGCGTCTTTCG 2554
QY 2493 TGAATTCAGATTGTTCTATGCAATCAGGAAGGTTTAAAGAACAGGGAACAGAGCTC 2552
Db 2555 TGAAGCTGAGTTTCTTATGCGCATCATGAATCTTTTACAGAGGAAGCGCATCAAGCTC 2614
QY 2553 GTGAATTCGAGTAGCCGCTCTGTGAATCTTGCCTTACTATCGGATCCGATTTGATA 2612
Db 2615 GGCATTCAGAGCGGACATCTCCTAAATCTATCAGTTCTCTGTGGAGTGAAGTTTGATC 2674
QY 2613 AGGAATCAGACTGCCAAGATGCAACCTGACATCTAATCTCTGTTATATCTGTGGATCTTG 2672
Db 2675 GATGTTCTAGTACACATCTCTAATAATATAGCTTTATGGCGGCTTATCTGTGATGCTT 2734
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QY 2673 TTCGTAGTAACCCCGACTGTACGACAAACACTGCAATTAGCGGTGATTTCTTGAAAACT 2732
Db 2735 ATCGCACCATTCTGTGTACTGAGACAAACGCTCTTATCCCATCAAGAGACATGACACAG 2794
QY 2733 TCGGTACGAATTTGGCAAGACAAAGCTTTAGTCCCTTCGTGTCAGGGAACCAATTTTGTGTTA 2792
Db 2795 ATGCGCTTTCAATTTAGCAAGACATGGAGTTGTGGTTAGAGGATCTATGTATGCTTCTCTAA 2854
QY 2793 ACTCAAAATTTGAAGCCTTTAGCCCAATTTCTTTTCAATTTGCGTGGTTCATCTCGCAAT 2852
Db 2855 CAAGTATATAGAGTATATGCCCATTGGAAGATATGAGTATCGAGATGCTTCTCGAGGCT 2914
QY 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTTCTAA 2887
Db 2915 ATGGTTGAGTCAGGAGTAAAGTCYGGTTCTAA 2949

RESULT 8
US-09-598-419-170
; Sequence 170, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-598-419-170

Query Match          4.4%; Score 131.4; DB 4; Length 2949;
Best Local Similarity 48.6%; Pred. No. 4.5e-28;
Matches 542; Conservative 2; Mismatches 523; Indels 48; Gaps 5;

QY 1776 TGACTCCAGATCCTATAATGGGTGAGAAATTCATTACGGCTATCAGGGAACCTTTGGGGCC 1835
Db 1880 TGACTCTAGGGAATGAGATGCCCTAAGTATGGCTATCAAGGAAGCTTGAAGCTTGGTGGG 1939
QY 1836 CAATTGTTGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAACCTGGCT 1895
Db 1940 ATCCTTAATACAGCAAAATATGGTCCCTTATFACCTCTGAAAGCTACATGGACTAAACCTGGCT 1999
QY 1896 ATATTCCTAATCCCGAGCGGTATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTTA 1955
Db 2000 ATAACTCTGGGCTGAGCGAGTAGCTCTTTGGTTCCAAATAGTTTATGGGATCCATTT 2059
QY 1956 TAGATATTAGCTCTCTCCATTATCTTATGGAGACTGCAAAACGAAGGGTTGCGAGGAGAC 2015
Db 2060 TAGATATACGATCTCGCATTCAGCAATTCAGCAAGTGTGGATGGCGCTCTTATTGTC 2119
QY 2016 GTGCTTTTGGTGTGCTGAGTATCTAATCTTCTCCATAGGATAGTACAAAACAGCAG 2075
Db 2120 GAGGATATGGGTTCTCGAGTTTCGAAATTTCTCTATCATGACCGCATGCTTTAGGTC 2179
QY 2076 GCGGTTTCGCCATTTGAGTGGCGGTATGTCAVAGGAGAAACCTACATACCTTTGTCAG 2135
Db 2180 AGGGATATCGGTATATTATAGTGGGGTATTCTTCTAGGAGCAAACTCTCTTTGGATCA- 2238
QY 2136 ATAAGATTCTTAGTCTGCAATTTTGTGAGCTTTTGGAGAGATAGAGACTACTTTGAG 2195
Db 2239 --TCGATGTTTGGTCTAGCAATTTACCGAAGTATTGGTAGATCTAAAGATTATGTAGTGT 2296
QY 2196 CTAAGAATCAAGGTACAGTCTACGAGGAACTCTCTATTACCAGCAACAGCAACCTATA 2255
Db 2297 GTCGTTCCAAATCATCATCTTGCATAGGATC-----CGTTTA 2333
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; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 169
; LENGTH: 2643
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-598-419-169

Query Match 1.7%; Score 50.6; DB 4; Length 2643;
Best Local Similarity 50.6%; Pred. No. 0.00018;
Matches 122; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
QY 1387 AGAGCGCGAGATTCTTAAATACTTCTGAGCTACTACAGCCTGTAACTCTTTTCAGG 1446
Db |||||
1218 AGAAGAAAAAATCTCTGATAACCTCACTTCCCACTACAGCAGCTATCGAACTGAAATC 1277
QY 1447 AGGTACTCTATCTTTAAACATGGAGTGTCTGACAGCTCAGGATTCACCTCAACAGGC 1506
Db |||||
1278 CGAAGCTTAGTTTAAAGATCGCGCTGTCTTCCGCGCTTCTCTCTCAGGATCC 1337
QY 1507 AGATTCTCGTCTCGAAATGGACGTAGCACTACTCTAGAACTGTCTGATAGTACCACT 1566
Db |||||
1338 TCAAGCTCTCTCTATTAAGAGCGGAACTCTTTTAAACATCTCTCTGATTTGAAGTT 1397
QY 1567 AAACAATTTGGTCAATTAACATCACTGTTCTATAGACGCTGCAAGAGGCAAAAATAGAAAC 1626
Db |||||
1398 AGCTACGCTAAGTATTCCTCTTCACTCTCTAGTACTGAAAAAGCGTAACTATCCACGC 1457
QY 1627 C 1627
Db 1458 C 1458

RESULT 12
US-09-556-877-181
; Sequence 181, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 181
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-181

Query Match 1.7%; Score 50.2; DB 4; Length 2601;
Best Local Similarity 50.2%; Pred. No. 0.00024;
Matches 121; Conservative 1; Mismatches 119; Indels 0; Gaps 0;
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Db |||||
1176 AGAAGAAAAAATCTCTGATAACCTCACTTCCCACTACAGCAGCTATCGAACTGAAATC 1235
QY 1447 AGGTACTCTATCTTTAAACATGGAGTGTCTGACAGCTCAGGATTCACCTCAACAGGC 1506
Db |||||
1236 CGAAGCTTAGTTTAAAGATCGCGCTGTCTTCCGCGCTTCTCTCTCAGGATCC 1295
QY 1507 AGATTCTCGTCTCGAAATGGACGTAGTACTCTAGAACTGTCTGATAGTACCACTATCCACGC 1566

Db 1296 TCAAGCTCTCTCTATTAAGAGCGGAACTCTTTTAAATACTCTCTTGTGATTTGAAGTT 1355
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QY 1627 C 1627
Db 1416 C 1416

RESULT 13
US-09-620-412C-181
; Sequence 181, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 181
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-181

Query Match 1.7%; Score 50.2; DB 4; Length 2601;
Best Local Similarity 50.2%; Pred. No. 0.00024;
Matches 121; Conservative 1; Mismatches 119; Indels 0; Gaps 0;
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Db |||||
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QY 1627 C 1627
Db 1416 C 1416

RESULT 14
US-09-598-419-181
; Sequence 181, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 181
; LENGTH: 2601
; TYPE: DNA

; ORGANISM: Chlamydia
US-09-598-419-181

Query Match 1.7%; Score 50.2; DB 4; Length 2601;
Best Local Similarity 50.2%; Pred. No. 0.00024;
Matches 121; Conservative 1; Mismatches 119; Indels 0; Gaps 0;

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| DB | 1176 | AGAGAGAAAACCTCTGATTAACCTCACITCCCACTACAGCAGCCTATCGAACTGAAATC | 1235 |
| QY | 1447 | AGGTACTCTATCTTTAAACATCGAGTGAATCTGCAGACTCAGGCATTCACCTCAACAGGC | 1506 |
| DB | 1236 | CGGACGCTTAGTTTAAAGATCGCGCTGCTCTTCCGSGCCTTCTCTCTCAGATCC | 1295 |
| QY | 1507 | AGATTCTGCTCGAAATGAGAGTGAAGTACTCTAGAACCTGTGATCTAGTACCAAT | 1566 |
| DB | 1296 | TCAAGCTCTCCTCATATTATGGAAGCGGAACCTCTTTAAAAAACTTCTCTVTGATTTGAAGTT | 1355 |
| QY | 1567 | AAACAATTTGGTCAATTAACATCAGTTCTATAGACGGTGCAGAGAGGCAAAATAGAAAC | 1626 |
| DB | 1356 | AGSTACGTAAGTATTCCTTCATCTCTTAGATACTGAAAAAGCGTAACATCCAGC | 1415 |
| QY | 1627 | C | 1627 |
| DB | 1416 | C | 1416 |

RESULT 15

US-08-213-419B-3/c
; Sequence 3, Application US/08213419B
; Patent No. 6333406

; GENERAL INFORMATION:
; APPLICANT: Inseiburg, J. et al.

; TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
; FILE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: J11-002CNCB

; CURRENT APPLICATION NUMBER: US/08/213,419B
; CURRENT FILING DATE: 1994-03-14

; PRIOR APPLICATION NUMBER: US 07/870,506
; PRIOR FILING DATE: 1992-04-17

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3
; LENGTH: 6124

; TYPE: DNA

; ORGANISM: Plasmodium falciparum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2407)..(2439)

; NAME/KEY: CDS

; LOCATION: (2598)..(3404)

; NAME/KEY: CDS

; LOCATION: (3580)..(3720)

; NAME/KEY: CDS

; LOCATION: (3850)..(5835)

; US-08-213-419B-3

Query Match

Best Local Similarity 1.4%; Score 42.4; DB 4; Length 6124;
Matches 76; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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| DB | 2288 | ATTATATTTTATTTTATTTTATTTTGGACATCTAAATTAATTTAAATTAATAATTTAT | 2229 |
| QY | 88 | TATATATTTTACATGAAGTCTCTTCCCCAAGTTTGATTTTCTACATTTGCTATTT | 147 |
| DB | 2228 | TATATATATATATATAAAATTAATAATAATATATATATATATTTAAATTTAATTT | 2169 |
| QY | 148 | CCCTTTGCTAT | 159 |
| DB | 2168 | TTATTTTAT | 2157 |

Search completed: December 16, 2003, 15:35:01
Job time : 175 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 12:20:54 ; Search time 885 Seconds

(without alignments)
11266.438 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 3000

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Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 546.6 | 18.2 | 2781 | 13 | US-09-738-269-56 |
| 3 | 546.6 | 18.2 | 2781 | 14 | US-10-023-437-56 |
| 4 | 506.6 | 16.9 | 3050 | 9 | US-09-452-380-1 |
| 5 | 506.6 | 16.9 | 3050 | 13 | US-10-324-129-1 |
| 6 | 477 | 15.9 | 2808 | 9 | US-09-452-380-2 |
| 7 | 477 | 15.9 | 2808 | 13 | US-10-324-129-2 |
| 8 | 348.4 | 11.6 | 2520 | 13 | US-09-738-269-22 |
| 9 | 348.4 | 11.6 | 2520 | 14 | US-10-023-437-22 |
| 10 | 271.8 | 9.1 | 2950 | 9 | US-09-886-468-6 |
| 11 | 218 | 7.3 | 4224 | 9 | US-09-841-132-486 |
| 12 | 148.2 | 4.9 | 487 | 13 | US-09-738-269-54 |
| 13 | 148.2 | 4.9 | 487 | 14 | US-10-023-437-54 |
| 14 | 132.2 | 4.4 | 3021 | 9 | US-09-841-132-182 |
| 15 | 131.4 | 4.4 | 2949 | 9 | US-09-841-132-170 |

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| 16 | 84 | 2.8 | 1745 | 9 | US-09-886-468-10 | Sequence 10, Appl |
| 17 | 82.2 | 2.7 | 2040 | 13 | US-09-738-269-52 | Sequence 52, Appl |
| 18 | 82.2 | 2.7 | 2040 | 14 | US-10-023-437-52 | Sequence 52, Appl |
| 19 | 81.4 | 2.7 | 2816 | 9 | US-09-886-468-8 | Sequence 8, Appl |
| 20 | 61.2 | 2.0 | 3050 | 10 | US-09-779-081-1 | Sequence 1, Appl |
| 21 | 61.2 | 2.0 | 4830 | 13 | US-09-841-260-59 | Sequence 59, Appl |
| 22 | 61.2 | 2.0 | 4830 | 14 | US-10-007-693-59 | Sequence 59, Appl |
| 23 | 55.8 | 1.9 | 379 | 13 | US-09-738-269-20 | Sequence 20, Appl |
| 24 | 55.8 | 1.9 | 379 | 14 | US-10-023-437-20 | Sequence 20, Appl |
| 25 | 51.2 | 1.7 | 5172 | 9 | US-09-841-132-374 | Sequence 374, Appl |
| 26 | 51.2 | 1.7 | 5172 | 9 | US-09-841-132-375 | Sequence 375, Appl |
| 27 | 50.6 | 1.7 | 2643 | 9 | US-09-841-132-169 | Sequence 169, Appl |
| 28 | 50.2 | 1.7 | 2601 | 9 | US-09-841-132-181 | Sequence 181, Appl |
| 29 | 45.2 | 1.5 | 591 | 13 | US-09-738-269-50 | Sequence 50, Appl |
| 30 | 45.2 | 1.5 | 591 | 14 | US-10-023-437-50 | Sequence 50, Appl |
| 31 | 44.2 | 1.5 | 3673778 | 13 | US-10-312-841-1 | Sequence 1, Appl |
| 32 | 43.6 | 1.5 | 12025 | 13 | US-10-311-455-1271 | Sequence 1271, Appl |
| 33 | 42 | 1.4 | 3673778 | 13 | US-10-312-841-2 | Sequence 2, Appl |
| 34 | 41.6 | 1.4 | 7049 | 13 | US-10-311-455-129 | Sequence 129, Appl |
| 35 | 41.6 | 1.4 | 7049 | 13 | US-10-240-452-5 | Sequence 5, Appl |
| 36 | 41.2 | 1.4 | 18997 | 13 | US-10-311-455-543 | Sequence 543, Appl |
| 37 | 41.2 | 1.4 | 18997 | 15 | US-10-172-086-17 | Sequence 17, Appl |
| 38 | 40.8 | 1.4 | 9539 | 13 | US-10-240-453-54 | Sequence 54, Appl |
| 39 | 40.8 | 1.4 | 9539 | 15 | US-10-239-676-52 | Sequence 52, Appl |
| 40 | 40.6 | 1.4 | 3048 | 13 | US-09-841-260-80 | Sequence 80, Appl |
| 41 | 40.6 | 1.4 | 3048 | 14 | US-10-007-693-80 | Sequence 80, Appl |
| 42 | 40.6 | 1.4 | 4190 | 13 | US-10-311-455-415 | Sequence 415, Appl |
| 43 | 40.2 | 1.3 | 18683 | 13 | US-10-311-455-286 | Sequence 286, Appl |
| 44 | 40.2 | 1.3 | 18683 | 13 | US-10-240-452-34 | Sequence 34, Appl |
| 45 | 40.2 | 1.3 | 24264 | 13 | US-10-017-161-665 | Sequence 665, Appl |

ALIGNMENTS

RESULT 1

US-09-428-122-1
; Sequence 1, Application US/09428122
; Publication No. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; APPLICANT: Mordin et al.
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 19721-007-019
; CURRENT FILING DATE: 1999-10-27
; EARLIER APPLICATION NUMBER: US/09/428.122
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/106,046
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/132,271
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3000
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(2884)
US-09-428-122-1

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| Query Match | 100.0%; | Score 3000; | DB 13; | Length 3000; |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | |
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| Db | 1 | CGCTCTACCTAGTAGAGGTTCGTAATTCCTGACTTCTCTATGCGTATCT | 60 | |
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| Db | 61 | CTTAAATATTAATTCAAATCAAGTATATTTTACAATGAGTCTTTTCCCAA | 120 | |

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QY 1861 TACGACTGCAACCTTCAACTGGACTTAAACCTGGCTATATTCCTAATCCGAGCGTATCGG 1920
Db 1861 TACGACTGCAACCTTCAACTGGACTTAAACCTGGCTATATTCCTAATCCGAGCGTATCGG 1920
QY 1921 CTCCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATAGCTCTCTCCATTAATCT 1980
Db 1921 CTCCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATAGCTCTCTCCATTAATCT 1980
QY 1981 TATGAGAGCTGCAAAACGAAGGGTTTCAGGGAGCCGCTGCTTTTGGTGTGCTGGATTATC 2040
Db 1981 TATGAGAGCTGCAAAACGAAGGGTTTCAGGGAGCCGCTGCTTTTGGTGTGCTGGATTATC 2040
QY 2041 TAACTCTTCCATAAGGATAGTACAAAAACAGACGGGGTTTCGCCATTTGAGTGGCGG 2100
Db 2041 TAACTCTTCCATAAGGATAGTACAAAAACAGACGGGGTTTCGCCATTTGAGTGGCGG 2100
QY 2101 TTATGCTCAGAGGAAACCTTACATCTTGTTCAGATTAAGATTTCTAGTCTGCAATTTTG 2160
Db 2101 TTATGCTCAGAGGAAACCTTACATCTTGTTCAGATTAAGATTTCTAGTCTGCAATTTTG 2160
QY 2161 TCAGCTCTTTTGAAGAGATAGAGACTACTTTGTAGTAAAGATCAAGGTACAGTCTACGG 2220
Db 2161 TCAGCTCTTTTGAAGAGATAGAGACTACTTTGTAGTAAAGATCAAGGTACAGTCTACGG 2220
QY 2221 AGGAACCTCTTANTTACAGCAACAGAAACCTTATCTCTCTTCTGCAAACTACGGCC 2280
Db 2221 AGGAACCTCTTANTTACAGCAACAGAAACCTTATCTCTCTTCTGCAAACTACGGCC 2280
QY 2281 TTGTTTGGTTGTTTATGTTCTTACAGAGATTCCTGTTCTCTTTTTCAGGAAAACTTAGCTA 2340

QY 508 TACCGCAAAGGAGCGGTTAGCTGCTACGGTAGCTTGTAGTTTGACAAAAATGTCTAG 567
Db 408 TACTGGAAGAGGGC---TATGAATCCGGAGGACATTAACCTTAGCGAATATATGCCAG 464
QY 568 TTGTCTCTCAGCAAAAACTTTTCAACGATAATGGCGGTGCTATCACCGCAAAAACCTCT 627
Db 465 TATTCTGTTTGTATCAGAATATTCCGCTGAGAATGGTGGAGCCATCTCTTGCAAGCTTT 524
QY 628 TTCAATACAGGAGTACAAATGTAGCTGCTGTTTCTGAAATATACCTCTCAAGAAAGG 687
Db 525 TTCTCTAACCGGCTCGAGCAAGAAATCAGCTTCAACCTAATCTACTGCGAAAAAGG 584
QY 688 CGGAGCCATTGAGACTTCGGATGCCCTTACCATTAATCTGAAACCAAGGGAAGTCTCTTT 747
Db 595 TGGAGCGATTGCTGCTACGGGAATAGCTCACTTTTCGACAAACCMAGGACAAATCAGATT 644
QY 748 TTCTGACAATATCTCTCGGATTTGGAGCTGCAATTTTTTACAGAAAGCTCGGTGACTAT 807
Db 645 TTCTGGGAACACTGCTGTGAATTTCTGGGGAGCAGTATATTACAGAAAGCTTCTATGACGAT 704
QY 808 TTCTAATATGCTAAAGTTTCTTTTATTGACAATPAAGTACAGGAGGAGCTCCTCAAC 867
Db 705 TGCAGGTAAACCAACGCTGCTTTTGTAGCAACAATGCTGTTTCCGGTTTCATCT----- 756
QY 868 AACGGGGATATGTGAGAGGTGCTATCTGTCTTATAAACTAGTACAGATCTAAGGT 927
Db 757 -----GATGGTTGCGGTGAGCTATCCATTTGACAAACAGGTTGAGCACCACCCCT 809
QY 928 CACCTCTACTGGAATCAGATGTTTACTCTTCAGCAACAATACATCGCAACAGCGGGAGG 987
Db 810 TACTATAAGATAACAAGTCTTGATTTTTGAGGAAAACTTCTTCAGCAAAAGGTGG 869
QY 988 AGCTATCTATGTGAAAAGCTCGAACTGCTTCGGAGGACTTACCTTATTCAGTAGAAA 1047
Db 870 AGCGAATTTACACCGATAAATCATATTGACTTCTGGTGGGCTACGGCAATTTATCAATA 929
QY 1048 TAGTGTCAATGAGGTACAGCTCTTAAAGGTGGAGCCATGCTATCGAAGATAGTGGGA 1107
Db 930 CAAAGTTACCATGCTACA----CTTAAGGTGGAGCTATTTGGTATTTGTCGCAATGGAGA 986
QY 1108 ATTGAGTTTAPCCGCCGATAGTGTGACATTTGTTTTTATGGGAA---TACAGTCACTTC 1164
Db 987 ATGTAGCTTAACCGCTGAACATGGGATATTACTTTTGATTAATAACCTGATGGCCACACA 1046
QY 1165 TACTACTCTGGAGGAATAGAAGTAGTATCGACTTAGGAACGAGTGAAGATGACAGC 1224
Db 1047 AGACAATGCTACATAAATAAAGAAATGCCAATTAACATTTGAAGGCAATGGTAAATTCGTCAA 1106
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Db 1107 CTTAGTGCAGCGTCTGGAAGACGATTTCTTTCTATGATCCTATCAGTTG----- 1159
QY 1285 CACAACAGTTACAGATGCTTTAAAGTTTAATGAGACTCCGGCAGATTCTGCACCTACAATA 1344
Db 1160 -----AAGGTAATGCTGCTGATCTTCTACCTTTGAATAAAGCTGAGGGTGAATAAACGTA 1214
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Db 1215 TAATGGAAGAAATTAATTTTTTCAGAGAAAAAGCTCACTGAAGAAACAAGTGTGTTGGGGA 1274
QY 1405 AAATCTTACTTCGAAGCTACTACAGCTGTAACTCTTTTCAGAGGCTACTCTATCTTTAAA 1464
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QY 1465 ACATGGAGTGACTCTGCAGACTCAGGCAATTCACCTCAACAGCAGGATTTCTGCTCTCGAAAT 1524
Db 1335 CAGCGGTGGAGTAGAAGCAAAAACAGTGTGTCGAACACAGCAGATCTTTGATCTTGAT 1394
QY 1525 GGACGTAGGAACCTACTCTA---GAACTGTGATACCTAGACCACTAAACAAATTTGGTCAT 1581
Db 1395 GGATGCGAGGCAAAAGTTATCCGCAAAAAACAGAAAGATGCTACACTGACGAATCTGGCTAT 1454
QY 1582 TAACATCAGTTCTATAGCGGTGCAAGAGGGCAAAAAATAGAACCAAGCTAGCTCAAA 1641

Db 1455 TAATCCGATACCTTTAGATGGAAAAAATTCGCGTAGTCGATGCCGTGCTGCTGGGAA 1514
QY 1642 AAATCTGACTTTATCTGGAACCATCACTTTATTGGAACCGGACGGGACGCTTTTATGAAA 1701
Db 1515 GAATGTGACTTTTATCAGGTGCTATTGGCGTTATTGATCCTACAGGGAAGTTTATGAAA 1574
QY 1702 TCATAGTTTAAAGAAATCTCAGTCTCAGCAGCATCTTAGAGCTCAAGGCTCTCGAACTGT 1761
Db 1575 CCATAAGCTAAATGATACGTTAGCTTTTAGGAGGAATCAACTTTCTGGAAAAAGTTCGGT 1634
QY 1762 AACAGCAGCAGCTGACTCCAGATCCTATAATCGGTGAGAAATTCATTTACGCTATCA 1821
Db 1635 GACAAACCAACGCTGCTAGTCACTGTTGGTGTGCTGTAACCCCACTATGTTATCA 1694
QY 1822 GGGAAAC-----TTGGGGCCCAATTTGTTGGGGACAGGGGCTCTACGACTGC 1869
Db 1695 AGGAAACTGGTCTGCTCAGTTGGGTCAAAGATAATAACTCTGATCCTAAACACAAACAGC 1754
QY 1870 AACCTTCAACTGGACTAAAACTGCTATATTCCTAATCCCGAGGCTATPCGGCTCTTTAGT 1929
Db 1755 AATCTTTACCTGGAAATAAAACAGGATATGTTCCAAATCCTGAACGCTGCTGCCGCTAGT 1814
QY 1930 CCCTAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCTCCATTTCTTATGAGAC 1989
Db 1815 ACTCAATAGCCTTTGGGATCCCTTTATAGATTTACGTTCTATTCAAGATGCTTTGGAACG 1874
QY 1990 TGCAAAACGAAGGTTGC---AGGGAGACCGTGTCTTTTGGTGTGCTCGAATTTCTAACTT 2046
Db 1875 TAGTGTGATAGTATTCTTGAGACACCTCGTGGTTGTGGGTCTCTGGAATTTGGAACCTT 1934
QY 2047 CTTCCATAAGGATAGTACAAAACACGACGCGGGTTTCGCCATTTGAGTGGCGGTATTGT 2106
Db 1935 CTTCCATAAAGATCGGAATGCTGAAAATCGAAAATCCGTATATCAGTTCGCGGATATGT 1994
QY 2107 CATAGGAGGAAACCTACATCTTCTCAGATAGATTTCTTAGTGTCTGCTATTTGTAGCT 2166
Db 1995 GTTAGGAGGACCAACAATACTCGAGAGAGGATTTCTTTAGTGTGGCTTTCTGCTCAGTT 2054
QY 2167 CTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAAATCAAGGTACAGTCTACGAGAGAAC 2226
Db 2055 ATTGCAAAAGATTAAGACTTACCTTTGTAAAGCAAGACGCGCAACGCTCTATGCGGGTTC 2114
QY 2227 TCTCTATTACAGCA-----CAACGAAACCTATATCTCTCTTCTTTCGAAACCTACGCCC 2280
Db 2115 TGTATATTATCAGCATGTAGCAAGTTTGTATGATCTCACGCGGTTATTTAATGGGCTAA 2174
QY 2281 TTGTTGCTGCTCTATCTTCTCAGAGATTCCTGTTCTCTTTTCAGAAACCTTAGCTA 2340
Db 2175 CAGGTGTTGTTTACGGGTTTCTAAAGAGATTCCTTATTTCTTGGATGCACAAATTTAGCTA 2234
QY 2341 CACCATAACGGATAACCGATCTGAAAAACCAAGTATACAAATATCTACTGTTTAAAGGAAG 2400
Db 2235 TTGCCACACGGCCACAAACATGACAGCTCTTATACAGACTATCTCTGAAGTGAAGGTTTC 2294
QY 2401 CTGGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGGAAAGCTCCGATTTGCTTTAGATGA 2460
Db 2295 TTGGGGTAATGATACATCCCTGGGCTTAACTTTGTCTACTAGCGTACCTATCCCGGTATTAG 2354
QY 2461 AAGTGTCTATTGAGGAGTACATGCGCTTCATGAATTTGCAATTTGCTCTATGACATCA 2520
Db 2355 TTCTTCTATCTTTGATAGTTTATGACCGTTTGCAAAATTTACAAAGTTGTCTATGCGCACCA 2414
QY 2521 GGAAGGTTTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGTAGCGCTCTTTGGA 2580
Db 2415 AGATGACTTTTAAAGAACCAACACAGAGCCGGGCTTTTGAAGCAGCGCATCTTCTCAA 2474
QY 2581 TCTTGCCTTACCTATCGGATCCGATTTGATAAGGAATCAGACTGCGCAAGATGCAACGTA 2640
Db 2475 CGTTTCTGTACCTATAGGTATATAAAATTTGAGAAACTCTCCTATGGAGAGAGAGTGTCTA 2534
QY 2641 CAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGTAAACCCGACTGTATGACAAAC 2700

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Db      2535 TGATCTTACACTGATGATATATACTGATGTGACCGTCATATCCAAAGCTGTATGACAGG 2594
Qy      2701 ACTGCGAATTAGCGGTGATTTCTTGGAAAAACCTTCGGTACGAATTTGGCAAGACAAGCTTTT 2760
Db      2595 ATTGGCGATCAATGACGTTTCTCGTTTAAACACACAGCTTACGAATCTTGTAGACAAGCTTT 2654
Qy      2761 AGTCCTTCGTCGAGGGAACCATTTTCTTTAACTCAAAATTTTGAAGCCCTTTAGCCAAAT 2820
Db      2655 CATAGTTTCGCGCGGTAAACAAATATGCTTAACTTCGGTGTGAGATGTTCACTCAGTT 2714
Qy      2821 TTCTTTTGAATTGCGTGGGTGATCTCGCAATTAACAATGTAGACTTAGGAGCAAAATACCA 2880
Db      2715 TGGTTTGAATTACGAAGCTCTTCAAGAAATTAACGTAGATCTTGGCGCTAAGTGGC 2774
Qy      2881 ATTCTAA 2887
Db      2775 GTTCTAA 2781

RESULT 4
US-09-452-380-1
; Sequence 1, Application US/09452380
; Patent No. US20020094340A1
; GENERAL INFORMATION:
; APPLICANT: MURDIN, Andrew D.
; APPLICANT: COHEN, Raymond P.
; APPLICANT: WANG, Joe
; APPLICANT: DUNN, Pamela
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; FILE REFERENCE: 032931/0216
; CURRENT APPLICATION NUMBER: US/09/452,380
; CURRENT FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3050
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(2908)
US-09-452-380-1

Query Match      16.9%; Score 506.6; DB 9; Length 3050;
Best Local Similarity 51.3%; Pred. No. 9.5e-131;
Matches 1473; Conservative 0; Mismatches 1324; Indels 72; Gaps 10;

Qy      66 AATATTAAATCAAAATCAAGTATATATTTTCAATGAAGTCTTCTTCCCAAGTTTG 125
Db      66 AATTTAATTTCTTGTTTCAAAAAGTCTTACAAATGAAGTCTCTCTCTCTTGTGTTG 125
Qy      126 TATTTTCTACATTTGCTATTTTCCCTT---TGCTATGATGCTACCGAGACAGTTTGG 192
Db      126 TCTTTTCTTCAATCCCGCTCTTTTCACTGCTCTCTATAGTCGCGGAGAGGTGACCTTAG 185
Qy      183 ATTCAAG---TGGAGTTTCGATGGGAATAAAAATGGAATTTTTCAGTTTCGTGAGATC 239
Db      186 ATAGCAGCAATAATAGCTATGATGATCTAACGGAACCTTCAACGCTCTTTTCCACTA 245
Qy      240 AGGAAGATGCT---GGAACTACCTATTTTAAAGGAAATGTCACTCTAGAAAAATATTC 296
Db      246 CGGACGCTGTGCGAGGAACCTACCTATTTCTTCTTCCGACGTATCTCTTCAAAATGCAG 305
Qy      297 CTGGAACAGCAGCAATCAAAAAGCTGTTTAAACAACACTAAGGGCGATTTGACTT 356
Db      306 GGGCTTTAGGAATTTCCCTTAGCCCTCAGGATGCTTCTTAGAAGCGGCGGCGATCTTACTT 365
Qy      357 TCACAGGTAACGGGAACCTCTTATTGTTTCCAAACGGTGGATGCGAGGACTGTAGCGGG 416

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Db      366 TCCAAAGAAATCAACATGCACTGAAGTTTGCATTTATCAATCGGGCTCTAGCGCTGGAA 425
Qy      417 CTGCTCTTTAACAGCAGCGTGGTAGATAAAATCTACCAAGTTTATAGGGTTTCTTCGCTAT 476
Db      426 CTGTAGCAGTACCTCAGCAGCAGATAAGAAATCTTCTTAAATGATTTTCTAGACTCT 485
Qy      477 CTTTATTTCGCTCTCTCGGAAAGTTTCGATAAATACCGGCAAGAGCGGTAGCTGCTCTA 536
Db      486 CTATTATCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 545
Qy      537 CGGGTAGCTTGAAGTTTGAACAAAATGTGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 596
Db      546 TGGGGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 605
Qy      597 ATAATGGCGGTGCTATCACCGCAAAAACCTCTTTTCAATACAGGACTCAAAATGTGAGCTC 656
Db      606 ATAACGGCGGTGTTATCAATACGAAAACCTTCTTATTATCAGGACATCTCAGTTTGGCA 665
Qy      657 TGTTTTCTGAAAATACCTCTCT-----CAAAGAAAGCGGAGCCATTCAGATTCGGATG 710
Db      666 GCTTTTTCGAGAAACCAAGCCTTTCACAGGGAAGCAAGCGGTGTAGTTTACGCTACAGGA 725
Qy      711 CCTTACCATTTACTGGAACCAAGGGAAGTCTCTTTTCTGACATATCTTCTCGATTT 770
Db      726 CTATAACTATCGAGAACAGCCCTGGGATAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 785
Qy      771 CTGAGCTGCAATTTTACAGAAAGCCTCGGTGACTATTTCTAATATGCTAAAGTTTCTCT 830
Db      786 CTGGCGTCTCTGTACACACTGACAACTGTTTCGATTACAGATAACTTTCAAGTATCT 845
Qy      831 TTATTGACAAATAGGTCACAGGAGGAGCTCTCTCAACAAACGGGGGATATGTCCAGGAGTG 890
Db      846 TTGACGGCAATAGTGTCTTGGGAAGCGGCTCAAGCTCAGGGCGGGGTAT----- 894
Qy      891 CTATCTGCTCTTATAAACTAGTACAGATACTAAAGTCACTCTCTCTCTCTCTCTCTCTCT 950
Db      895 -----TTGTTGCACTACAGACATAAACAAGTGACTCTTCTCTGGAACAAAAACC 944
Qy      951 TACTCTTCAGCAACATATACATCGACAAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCG 1010
Db      945 TCTCTTTTCAAAATAATACAGATTGACATATGCGGAGCCATCTCTGACTCAGGTCA 1004
Qy      1011 AACTGCTTCCGGAGACTTACCTTATTCAGTAGAAATAGTGTCAATGAGGATCAGCTC 1070
Db      1005 GTATTTCCGCTGGAGGTCTCTCTCTATTTTCAAAAGTAATATCTCAGGAAGTAGCGCGGTC 1064
Qy      1071 ---CTAAAGTGGAGCCATAGCTATCGAAGATAGTGGGAATTTGAGTTTATCGCGGATA 1127
Db      1065 AGGAGGAGGAGGAGGAGTCAATATAGCATCTGTGGGAACTCGCTCTCTCTCTCTCTCT 1124
Qy      1128 GTGGTGACATTTGCTTTTGGGAATACAGTCACTTCTACTACTCTCTGGAAGCAATAGAA 1187
Db      1125 CTGGAGATATTACCTTCAATAACCAAGTCAACAAAGCAAGCAAGTACAAAGAAACG 1184
Qy      1188 GTAGTATCACTTAGGAACGAGTGCAGAGATGACAGCTTTTGGCTTCTGCTGTGTAGAG 1247
Db      1185 CAATAAATATCAATTGATAC---CGCTAAAGTCAATCGATACGAGTGTCTAGCGGCAAT 1241
Qy      1248 CCATCTTCTCTATGATCCCAATCTACAGGATCACTCCCAACAGTTACAGATGCTCTAA 1307
Db      1242 CTATCTATTCTTATGATCCCATCAAAATCCAGGAACCGAGCTTCTACCGACATGGA 1301
Qy      1308 AAGTTAATGAGACTCGGCAGATTTGCACTACAATATACAGGGAACTCATCTTTCAAG 1367
Db      1302 ACTTAACTTAGCAGATGGAACAGTGAATCGAGTATGGGGTGGGATTTGCTTTCTG 1361
Qy      1368 GAGAAAGTTATCAGAGACAGAGCGCGGAGATTTTAAAAATCTTACTTGAAGCTACTAC 1427
Db      1362 GAGAAAGCTTTTCCCTTACAGAAAAAGCAATCGCTGCAAAACGCTCTCTACTATCCGAC 1421
Qy      1428 AGCTGTAACTCTTTTTCAGGAGGTACTCTATCTTTTAAACATGAGTGTCTGACAGCTC 1487

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Db 1422 AACCTGCAGTATTAGCGGGGAGACTCTTGTAATCTTGATGGAGTACACCGTACTTTCA 1481
QY 1488 AGGCAATTCACCTACAGCAGCAATCTCGTCTCGAAATGGAGCTAGGAACCTACTCTAGAAC 1547
Db 1482 AGGATCTGACTCAAAGTCCAGGATCCCGCATCTTAATGGATGGGGGACTACACTTAGTG 1541
QY 1548 CT---GCTGATPACTAGCACCATAAACAATTTGGTCATTAAACATCAGTTCTATAGACGGTG 1604
Db 1542 CTAAGAGGCAATCTTTGGCTTAATGGCTTAGCAGTAATCTCTCTCTTTAGATGAA 1601
QY 1605 CAAAGAGGCAAAATAGAAACCAAGCTACGTCAAAAAATCTGACTTTTATCTGGAACCA 1664
Db 1602 CCAACAGGAGCTTTAAACACAGAGCTGCAGATAAAAAATATCAGCTATCGGGAACGA 1661
QY 1665 TCACCTTTATGGACCGGACGGCAGTTTATGAAATCATAGTTTAAAGAACTCCTCAGT 1724
Db 1662 TTGGCGCTTAITGGACCGGAAAGGGTCATCTATGAGAATCAAACTTAAAGATGCTAGTA 1721
QY 1725 CCTACGACATCTTAGAGCTCA-----AAGCTTCTGGAACCTGTAAACAGCACCCGAG 1775
Db 1722 CCTATCCTCTCTTGAACCTACACCGGAGGACCAACGGAACGATTAATCTCGGAGCTC 1781
QY 1776 TGACTCCAGATCCCTAATATGGGTGAGAAATCCATTAACGGCTATCAGGGAACCTTTGGGCCC 1835
Db 1782 TTTCTACCTGACTCTTCAAGAACCTGAAACCCACTACGGGTATCAAGGAACTGGCAGT 1841
QY 1836 CAATTTGTTGGGGACAGGGGCTTCTAGGACTGCAACCTTCAACTGACTAAAACTGGCT 1895
Db 1842 TGTCTTGGGCAAAATGCAACATCTCTCAAAAAATAGGAGCATCAACTGGACCGGTACAGGAT 1901
QY 1896 ATATTCCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTTAATAGCTTATGGAATGCATTTA 1955
Db 1902 ACATTCCTAGTCTGAGAGAAAGTAATCTCCCTCTAATATAGCTTATGGGAACTTTA 1961
QY 1956 TAGAATTAAGCTCTCTCCTATATCTTATGAGACTGCAAAACGAGGGTTGCGAGGAGACC 2015
Db 1962 TAGATATACGCTGATCAATCAGCTTATAGAAACCAAGTCCAGTGGGAGCCCTTTGAGC 2021
QY 2016 GTGCTTTTGGTGTGCTGGATATCTAACTTCTTCCATAGGATAGTACAAAAACAGCAC 2075
Db 2022 GTGAGCTATGCTTTTCAGGAATTCGGAATTTCTTCTATAGAGATTCATGCCACCCGCC 2081
QY 2076 GCGGGTTTGCATTTGAGTGGGGTATGTCATAGGAGGAAACCTACATACATGTTTCAG 2135
Db 2082 ATGTTTCCGCCATATCAGCGGGGTTATGCACTAGGGATCAAGCAACACTCCTCCGC 2141
QY 2136 ATAAGATCTTAGTGTGCTATTTTGTGAGCTCTTTGGAAGAGATAGAGACTACTTTGTAG 2195
Db 2142 AGGATCAGCTTACTTTTGGCTTCTGCCAGCTCTTTGCTAGAGATCGCAATCATATTACAG 2201
QY 2196 CTAAGATCAAGGTACAGTCTACGGAGAGACTCTCTATTACGAGC----- 2240
Db 2202 GTAAGAACCCAGGAGATPACTTACGGTCCCTCTTTGATTTCCACCATACAGAAGGGCTCT 2261
QY 2241 ---ACACGAAACCTATATCTCTCTTCTGCAAACTACGGCTTGTCTGTTCTATG 2297
Db 2262 TCAGATCGCCCAATTTCTCTGGGAAAAGCAACCCGAGTCCCTGGGTCTCTCTGAGA 2321
QY 2298 TTCTCAGAGATTCCTGTTTCTCTTTTCAGGAACCTTTAGCTACACCCATACGGATAACG 2357
Db 2322 TCTCCAGATCATTTCTTTATCGTTGATGCTAAATTCAGTTATCTCCATACAGCAACC 2381
QY 2358 ATCTGAAAACCAAGTATACAAATATCCTACTGTTTAAAGGAAGCTGGGGAATGATAGTT 2417
Db 2382 ACATGAAGACATATTATACCGGATAACTCTATCATCAAGGGTCTTCTGGAGAAACGATCCCT 2441
QY 2418 TCGCTTTAGATTCGGTGGAGAGCTCCGATTTGCTTAGATGAAGTGCTCTATTGAGC 2477
Db 2442 TCTGTGAGATCTTGGAGTAGCTGCTTTGTTATTTCCGTTCCGATATCTCTGAAAG 2501
QY 2478 AGTACATGCCCTTCATGAAATTCAGTTTCTGATGCAATCATCAGGAAGGTTTAAAGAAC 2537
Db 2502 AAGTCGAACCTTTGTCAAAGTACAGTATATATATGCGCATCAGCAAGACTTCTACGAGC 2561

QY 2538 AGGAAACAGAGCTCGTGAATTTGGAAATAGCCGTCTTGTGAATCTTTCCTTACCTATCG 2597
Db 2562 GTCATGCTGAAGACGCGCTTTCAATAAAAGCGAGCTTATCAACGTAGAGATTCCTATAG 2621
QY 2598 GGAATCCGATTTGATAGGAATCAGCTGCCAAGATGCAAGTACAAATCTAACTCTTGGTT 2657
Db 2622 GCGTCACTTCGAAAGAGACTCAAAATCAGAAAGGGAATTAAGATCTTACTCTTATGT 2681
QY 2658 ATACTGTGATCTTTGTTCTGTAGTAACCCGACTGTACGACAACTCGGAATTAGCGGTG 2717
Db 2682 ATATACTCGATGCTTACCGACGCAATCTTAATGTCAAATCTCCCTAATAGCTAGCGATG 2741
QY 2718 ATCTTGGAAAACTTCGGTACGAATTTGGCAAGAAGAAGCTTTAGTCTTTCGTGACGGA 2777
Db 2742 CTAACGTGATGGCTATGTTACCAACCTCGCACGACAAAGGTTTTTCTGTTCGTGTCGA 2801
QY 2778 ACCATTTTCTTTAACTCAAAATTTTGAAGCCTTTAGCCAAATTTCTTTGAAATTCGCTG 2837
Db 2802 ACCATTTCCAGTGAACCCCAACATGGAATCTTCGGTCAATTCGCTTTTGAAGTACGAA 2861
QY 2838 GGTCACTCTCGCAATTAATAGTGTAGCTTAGGAGCAAAAATACCAATTTCTA 2886
Db 2862 GTTCTTCAAGAAATTAATATACAAACCTAGGCTCTAAGTTTGTCTTA 2910

RESULT 5

US-10-324-129-1
; Sequence 1, Application US/10324129
; Publication No. US20030157124A1
; GENERAL INFORMATION:
; APPLICANT: Mordin et al.
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses the
; FILE REFERENCE: 77813-4
; CURRENT APPLICATION NUMBER: US/10/324,129
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3050
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(2908)
US-10-324-129-1

Query Match 16.9%; Score 506.6; DB 13; Length 3050;
Best Local Similarity 51.3%; Pred. No. 9.5e-131;
Matches 1473; Conservative 0; Mismatches 1324; Indels 72; Gaps 10;

QY 66 AATATTAAATTCAAAATCAAAGTATATATTTTACAATGAAGTCTTCTTTCCCAAGTTTG 125
Db 66 AATTAAATTCCTTGTTCAAAAAGTCTTACAAATGAAGTCTCTGTCTCTTGTGTGT 125
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Db 126 TCTTTTCTTCAATCCCGCTCTTTTTCATCGCTCTCTATAGTCGCGGAGAGGTGACCTTAG 185
QY 183 ATTCAAG---TGGAGTTCGATGGGAATAAAAAATGTAATTTTTCAGTTTCGTGAGATC 239
Db 186 ATAGCAGCAATAATAGCTATGATGATCTTAACGGAACCTACCTTCACGGTCTTTTCCACTA 245
QY 240 AGGAAGATGCT---GGAACCTACCTACTATTTTAAAGGGAATGTCACTCTAGAAAAATTC 296
Db 246 CGGACGCTGCTGCGGAACCTACCTATTCCTTACTTCTCCGAGGTATCCTTCTCAAAATGCGAG 305
QY 297 CTGGAACAGGCACAGCAATCAACAAAAGCTGTTTAAACACACTAAGGGCGATTTGACTT 356

Db 306 GGGCTTTAGGAATCCCTTAGCTCAGGATCGTTCCTTAGAGCGGCGCGATCTTACTT 365
Qy 357 TCACAGGTAAACGGGAACCTCTTATTTGCCAAACGGTGGATGACGGAGCTGTAGCAGGG 416
Db 366 TCCAAGGAAATCAACATGCACTGAAGTTTGCAATTTATCAATGCGGGCTCTAGCGCTGGAA 425
Qy 417 CTGCTGTTAAACAGCAGCGTGGTGAATAATCTACCAAGTTTATAGGGTTTCTCGCTAT 476
Db 426 CTGTAGCCAGTACCTCAGCAGCAGATAAGAACTCTCTCTTAATGATTTTTCTAGACTCT 485
Qy 477 CTTTTATTGCGTCTCCTGGAAGTTCGATAAATACCGCAAGCGGCGGTAGCTCTCTTA 536
Db 486 CTAATATCTCTGTCCT 545
Qy 537 CGGGTAGCTTGAAGTTGACAAAATATGTCAGTTTGTCTCTCTCTCTCTCTCTCTCTCT 596
Db 546 TGGGAAATCTATCTCTAATGCGCAATTCCTCAAAATATATTTACTCAGAACTTCTCGTCAG 605
Qy 597 ATAATGGCGTCTATCACCGCAAAATCTTTCTTCAATTAACAGGACTACAATGTCAGTCT 656
Db 606 ATAACGGCGGTGTTATCAATACGAAATCTCTTATATCAGGGACATCTCAGTTTGGGA 665
Qy 657 TGTCTTCTGAAATACCT 710
Db 666 GCTTTTCGAGAAACCAAGCTTTCAGAGGAACGAGCGGTGTAGTTTACGCTACAGGAA 725
Qy 711 CCCTTACATTAATGGAACCAAGGGAGTCTCTTTTCTGACAAATCTTCTCGGAT 770
Db 726 CTATAACTATCAGAAACAGCCCTGGGATAGTTTCTCTCTCTCTCTCTCTCTCTCTCT 785
Qy 771 CTGGAGCTCAATTTTACAGAAGCTCGTGACTATTTCTAATATGCTAAAGTTTCTCT 830
Db 786 CTGGCGGTCTCTGTACAGACTGTACAACCTGTTCTGATTAACAGATTAATCTTCAAGT 845
Qy 831 TTATTGACAAATAGGTTCAGAGGAGCTCTCTCAACAAACGGGGATATGTTCAGAGGTG 890
Db 846 TTGACGGCAATAGTCTTGGGAACGCTCAAGCTCAGGCGGGGCTAT- - - - - 894
Qy 891 CTATCTGTGCTTATAAACTAGTACAGATCTAAGTTCACCTCTCAGTGGAAATCAGATGT 950
Db 895 - - - - - TTGTTGCACTACGACAGATAAACAACAGTGACTCTTACTGGGAACAAAAACC 944
Qy 951 TACTCTCAGCAACATATACACAAACAGCGGAGGACTATCTATGTGMAAAGCTCG 1010
Db 945 TCTCTTTCAAAATAACAGATTCAGATATGCGGGAGCCATCTCTGCACTCAGGTCA 1004
Qy 1011 AACTGGCTTCCGAGGACTTACCCTATTCCAGTAGAAATAGTGTCAATGAGGATCAGCTC 1070
Db 1005 GTATTTCCGCTGGAGTCTCTCTATTTTCAAAATATATCTCAGGAAGTAGCGCGGTC 1064
Qy 1071 - - - - - CTAAAGTGGAGCCATAGTATCGAAGATAGTGGGAATGAGTTTATCGCGGATA 1127
Db 1065 AGGGAGGAGGAGGAGGATCAATATATAGCATCTGCTGGGGAATCGCTCTCTGTCTACTT 1124
Qy 1128 GTGGTGACATGTCTTTTGGGAATACAGTCACTTCTACTCTCTGGGAGCAATPAGAA 1187
Db 1125 CTGGAGATATATACCTTCAATAACCAAGTACCAAGTACCAAGCAAGTACAGAAACG 1184
Qy 1188 GTAGTATCGACTTAGGAACGAGTGCAGAAATGACAGCTTTTGGCTTCTGTCTGTAGAG 1247
Db 1185 CAATAAATATATTGATAC- - - - - CGCTAAAGTACATCGATACAGCTGCTACGGGCAAT 1241
Qy 1248 CCACTCTACTTATGATCCCATTAATCTACAGGATCTCCACACAGTTACAGATGCTTAA 1307
Db 1242 CTATCTATTCTATGATCCCATCACAAATCCAGGAACCGCAGCTTCTACCGACACATGA 1301
Qy 1308 AAGTTAATGAGATCCCGGAGATTTCTGCACTACAATATACAGGAACATCTCTCACAG 1367
Db 1302 ACTTAACTTAGCAGATGCGAACAGTGAATCGAGTATGGGGTGGATGTCTTTCTG 1361
Qy 1368 GAGAAAGTTTATCAGACAGAGCGCGCAGATTTCTAAAAATCTTACTTCGAAGCTACTAC 1427
Db 1362 GAGAAAGCTTTCCCTTACAGAAAGCAATCGCTGMAACGTCACCTCTACTATCCGAC 1421

Qy 1428 AGCTGTAACTCTTTTCCAGAGGTACTCTATCTTTTAAACATGAGTGACTCTCTCAGACTC 1487
Db 1422 AACCTGCAGTATTTAGCGGGGAGATCTTGTACTTTCGTGTAGTGGAGTCAACCGTAATTTCA 1481
Qy 1488 AGGCATTCACCTCAACAGCAGATTTCTGTCTCGAAATGGAAGTAGGAACTACTCTAGAAC 1547
Db 1482 AGGATCTGACTCAAGTCCAGATCCCGCATCTTTAATGGATGGGGGACACTACTTAGTG 1541
Qy 1548 CT- - - - - GCTGATCTAGCACCAATAAACAATTTGGTCAATTAACATCAGTTTCTATAGCGGTG 1604
Db 1542 CTAAGAGGCAAACTCTTTCGCTTAATGGCTTAGCAGTAAATCTCTCTCTTTTAGATGAA 1601
Qy 1605 CAAGAAGGCAAAATAGAACCAAGCTAGCTCAAAAATCTGACATTTATCTGGAACCA 1664
Db 1602 CCAACAGGAGCTTTTAAAAACGAAGCTGAGATAAAAAATCAGGCTATTCGGGAACGA 1661
Qy 1665 TCACCTTTATGGAACCGGACGCTTTTATGAAATCATAGTTTAAAGAAATCCTCAGT 1724
Db 1662 TTGGCTTATTTGACACGGAAGGTCTATCTATGAGATCAATCTTAAAGTGTCTAGTA 1721
Qy 1725 CTTAGCAGATCTTAGAGCTCA- - - - - AAGCTTCTGGAACCTGTAAACAGCACCGCAG 1775
Db 1722 CTTATCTCTCTTTTGAACCTTACACCGCAGGAGCCACGGAACGATTTACTCTGGAGCTC 1781
Qy 1776 TGACTCCAGATCTCTATATGAGTGAATTTCCATTTACGGCTATCAGGAACTTTGGGSC 1835
Db 1782 TTTCTACCTGACTCTTCAAGAACTGAAACCCACTACGGGTATCAAGGAACTGGCAGT 1841
Qy 1836 CAATTGTTTGGGGACAGGGGCTCTTACGACTGCAACCTTCAACTGGACTAAAACTGGCT 1895
Db 1842 TGTCTTGGGCAATTCGAACATCTCTCAAAATAGGAGCATCAACTGGACCCGTACAGAT 1901
Qy 1896 ATATCTTAATCCGAGGCTATCGGCTCTTTTGTCTCTTAATAGCTTATGGAATGCAATTA 1955
Db 1902 ACATTCTCTAGTCTCTGAGAGAAAAAGTAACTCTCCCTCTAAATAGCTTATGGGAAAACTTTA 1961
Qy 1956 TAGATATTAGCTCTCTCCATTTCTTATGAGAGCTGCAAAACGAAGGTTTCAGGAGAC 2015
Db 1962 TAGATATACGCTCGATCAATCAGCTTATAGAAACCAAGTCCAGCTGGGGAGGCTTTTGAGC 2021
Qy 2016 GTGCTTTTGTGTGCTCGATTTCTAACTCTTCTCAATAGGATAGTACAAAAACAGAC 2075
Db 2022 GTGACTATGCTTTCAGGAATTTGGAATTTCTTCTATAGAGATTCATGCCACCCGCC 2081
Qy 2076 GCGGTTTTCGCAATTTAGTGGCGGTATGTCATAGGAGGAAACCTACATCTTGTTCAG 2135
Db 2082 ATGGTTTCCGCCATATCAGCGGGGTTATGCACTAGGGATCACAGCAACACTCTGCGC 2141
Qy 2136 ATAAGATTTCTAGTCTGCATTTTGTGCTCTTTTGGGAAGATAGAGACTACTTTGTAG 2195
Db 2142 AGGATCAGCTTACTTTTGTCTCTCCAGCTTTTGTCTAGAGATCGCAATCATATTACAG 2201
Qy 2196 CTAAGAAATCAAGGTACAGTCTACGGAGGAACCTCTCTATTACCAGC- - - - - 2240
Db 2202 GTAAGAACCAAGGAGATCTTACGGTCTCTTTCTTATTTCCACCATACAGAGGCTCT 2261
Qy 2241 - - - - - ACAAAGAAACCTATATCTCTCTCTTTCGAAACCTAGGGCTTGTCTTGTATG 2297
Db 2262 TCGACATCGCAATTTCTCTGGGAAAAAGCAACCGAGCTCCCTGGGTGCTCTCTGAGA 2321
Qy 2298 TTCTCTACAGATTTCTCTCTCTTTTTCAGGAAACCTTAGCTACACCCATCGGATAACG 2357
Db 2322 TCTCCAGATCATTTCTTTTATGCTGCTGATGCTAAATTCAGTTATCTCCATACAGCAAC 2381
Qy 2358 ATCTGAAAAACCAAGTATACACATCTCTACTGTTTAAAGGAGCTGGGGAAATGATGTT 2417
Db 2382 ACATGAGACATATTTATACCGATTAATCTATCATCAGGGTTCTTTGGAGAAACGATGCT 2441
Qy 2418 TCGCTTTAGAAATTCGGTGAAGAGCTCCGATTTGCTTGTAGTGAAGAGTCTTATTGTAGC 2477
Db 2442 TCTGTGCAGATCTTGGAGCTAGCCTGCTTTTGTATTATTTCCGTTCCGTATCTTCTGAAAG 2501

| | | | |
|----|------|--|------|
| QY | 1402 | TAAAAATCTTTACTTCGAAGCTACTACAGCCTGTAACTCTTTTCAGGAGGTACTCTATCTTT | 1461 |
| DB | 1297 | TGCAAAACGTACACCTCTACTATACGACAACCTGCAGATTATTAGCGCGGGAGATCTTGTA | 1356 |
| QY | 1462 | AAAACATGGAGTAGCTCTGCAGACTCAGGCAITTCACCTCAACAGCGCAGATTCCTCGTCTCGA | 1521 |
| DB | 1357 | TCGTGATGGAGTCACCGTAACTTTCAAGGATCTGACTCAAAGTCCAGGATCCCGCATCTT | 1416 |
| QY | 1522 | AATGGACGTAGGAACACTCTCTAGAACCT---GCTGATACTAGCACCAATAAACAATTTGGT | 1578 |
| DB | 1417 | AATGGATGGAGGATACACTTAGTGTAAAGAGGCAATCTTTTCGCTTAATGGCTTAGC | 1476 |
| QY | 1579 | CATTAAACATCAGTTTCTATAGACCGTGCAAAAGAGGCAAAAATAAGAAACCAAGACTACGTC | 1638 |
| DB | 1477 | AGTAAATCTCTCTCTCTTTAGATGAACCAACAAGGCAGCTTTAAAAACAAGACGTGCAGA | 1536 |
| QY | 1639 | AAAAAATCTGACTTTATCTGGAACCATCACTTTATGGACCGACGGCAGCTTTTATGA | 1698 |
| DB | 1537 | TAAAAATATCAGCCTATCGGGAACGATTCGGCTTTATTGACACGGAAGGGTCATTCTATGA | 1596 |
| QY | 1699 | AAATCATAGTTTAAAGAAATCCTCAGTCCTCAGCATCTTAGAGCTCA-----AAGC | 1749 |
| DB | 1597 | GAATCATAACTTTAAAAAGTGTGTAAGTCTATCTCTTCTTCTTGTGAATTTACACCGCAGGAC | 1656 |
| QY | 1750 | TTCTGGAACTGTAAACAAGCACCGCAGTGACTCCAGATCCTATAATGGTGAGAAATTC | 1809 |
| DB | 1657 | CACCGAACGATTACTCTGGGAGCTCTTTCTTACCCTGACTCTTCAAGAACCTGAAACCCCA | 1716 |
| QY | 1810 | TTACGGCTATCAGGAACCTTGGGGCCCAATTTGTTGGGGACAGGGGCTCTTACGACTGC | 1869 |
| DB | 1717 | CTACGGGTACAAAGGAAATCGCAGTTGTCTTGGGCAAAATG-CAAACATCTTCAAAAATPAGG | 1775 |
| QY | 1870 | AACCTTCAACCTGGACTAAACCTGCTATATTCTTAATCCCGAGCGTATCGGCTCTTTAGT | 1929 |
| DB | 1776 | AAGCATCAACTGGACCCGTACAGGATACATTCCTTAGTCCTGAGAGAAAAAGTAACTCTCCC | 1835 |
| QY | 1930 | CCCTAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCTCCATTAATCTTATGGAGAC | 1989 |
| DB | 1836 | TCTAATATAGCTTATGGGAAACTTTTATAGATATACGTCGATCAATCAGCTTATAGAAAC | 1895 |
| QY | 1990 | TGCAACGAAGGGTTGCAGGAGACCGTGCTTTTGGTGTGCTGGATTATCTAACTTCTTT | 2049 |
| DB | 1896 | CAAGTCCAGTGGGAGCCTTTTGAGCGTGAGCTATGGCTTTTCAGGAATTCGGAATTTCTT | 1955 |
| QY | 2050 | CCATAAGGATAGTACAAAACACAGACGGGCTTTGCGCAITTTGATGTGCGGTTATGTCAT | 2109 |
| DB | 1956 | CTATAGAGATTCTATGCCCCACCCGCCATGGTTTCGCCCATATACGCGGGGGTTATGCAC | 2015 |
| QY | 2110 | AGGAGGAAACCTACATACTTGTTCAGATAAGATTCTTAGTGCTGCATTTTGTCTCAGCTCTT | 2169 |
| DB | 2016 | AGGGATCACAGCAACAATCTCTCGGAGGATCAGCTTACTTTTGCTTCTGCCAGCTCTT | 2075 |
| QY | 2170 | TGGAAGAGATAGAGACTACTTTGTAGCTAAGAAATCAAGGTACAGTCTACGGAGGAACTCT | 2229 |
| DB | 2076 | TGCTAGACATCGCAATCATATTACAGGTAAAGAACCCAGGAGATCTTTACCGTGCCTCTTT | 2135 |
| QY | 2230 | CTATTACCAGC-----ACAAAGAAACCTTATATCTCTCTCTCTCTCTTCCCTTGC | 2271 |
| DB | 2136 | GTAATTTCCACCANTACAGAAGGGCTCTTCGCATCGCCAAATTCCTCTCGGGGAAAAGCAAC | 2195 |
| QY | 2272 | ACTACGGCTTGTTCGTTGTCTTATGTTCTTACAGAGATTCTCTTCTCTTTTTCAGGAAA | 2331 |
| DB | 2196 | CGAGCTCCCTCGGGTGCTCTTGAGATCTCCAGATCAATCTCTTTATCGTTCGATGCTAA | 2255 |
| QY | 2332 | CCTTAGCTACACCCATACGGGATACGATCTGAAAACCAAGTATACAAATATCTCTACTGT | 2391 |
| DB | 2256 | ATTCACTTATCTCCATACAGCAACCAATGAAGACATATTATACCGATAACTCTATCAT | 2315 |
| QY | 2392 | TAAAGGAAGCTGGGGGAATGATAGTTTCGTTTGAATTCGGTGGAGAGAGCTCCGATTTG | 2451 |
| DB | 2316 | CAAGGGTCTTGGAGAAACGATGCCTTCTGTGCAGATCTTGGAGCTAGCCTGCTTTTGT | 2375 |

| | | | | |
|---|----|------|--|------|
| | QY | 2452 | CTTAGATGAAGAAGTCTCTATTGTCAGCAGTACATGCCCTTCATGAAATTCGAGTTTGCTTA | 2511 |
| | Db | 2376 | TATTTCCGTTCGGTAACTTCTGAAAGAAAGTCGAACCTTTTTGTCAAAGTACAGTATATCTA | 2435 |
| | QY | 2512 | TGCACATCAGGAAGGTTTTAAAGAACACAGGGAACAGAAAGCTCGTGAAATTTGGAGTAGCCG | 2571 |
| | Db | 2436 | TGGCATCAGCAAGACTTCTACGAGCGTCATGCTGAAGAGACGGCTTTCATAAAAAGGGA | 2495 |
| | QY | 2572 | TCTGTGGAATCTTTGCCCTTACCCTATCGGGATCCGATTTGATAAGGAATCAGACTGCCAAGA | 2631 |
| | Db | 2496 | GCTTATCAACGTAGAGATTCTTAGCGCTCACCTTCGAAAGAGACTCAAAATCAGAAAA | 2555 |
| | QY | 2632 | TGCAACGTACAATCAACTCTTGGTTATCTGTGGATCTTGTTCGTAGTAAACCCGACTG | 2691 |
| | Db | 2556 | GGGAACCTTACGATCTTACTCTTATGTATATACGTATGCTTACCGACGCAATCCCTAAATG | 2615 |
| | QY | 2692 | TACGACAACACTGCGAATFAGCGTGATCTTGGAAAACCTTCGGTACGAAATTTGGCAAG | 2751 |
| | Db | 2616 | TCAAACTTCCCTAATAGCTAGCAGATCTACTGGATGGCTATGGTACCACTTCGCACG | 2675 |
| | QY | 2752 | ACAAGCTTTAGTCCCTTCGTGACAGGAAACCAATTTTGTCTTAACTCAAATTTGAAGCCTT | 2811 |
| | Db | 2676 | ACAAGGTTTTCTGCTCGTGCAGAACCAATTTCCAAGTGAACCCACATGGAATCTT | 2735 |
| | QY | 2812 | TAGCCAAATTTCTTTGAATTCGGTGGTCACTCTCGCAATTAACAATGTAGACTTAGGAGC | 2871 |
| | Db | 2736 | CGGTCAATTCGCTTTTGAAGTACGAAAGTTCTTTCACGAAATTTATAATACAAACCTTAGGCTC | 2795 |
| | QY | 2872 | AAAAT 2876 | |
| | Db | 2796 | TAAAT 2800 | |
| RESULT 7 US-10-324-129-2 ; Sequence 2, Application US/10324129 ; Publication No. US20030157124A1 ; GENERAL INFORMATION: ; APPLICANT: Murdin et al. ; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and v ; FILE REFERENCE: 77813-4 ; CURRENT APPLICATION NUMBER: US/10/324,129 ; CURRENT FILING DATE: 2002-12-20 ; PRIOR APPLICATION NUMBER: US 60/113,439 ; PRIOR FILING DATE: 1998-12-01 ; PRIORITY CLAIMING DATE: 1998-12-01 ; PRIOR FILING DATE: 1999-05-03 ; NUMBER OF SEQ ID NOS: 6 ; SOFTWARE: Patent In Ver. 2.0 ; SEQ ID NO 2 ; LENGTH: 2808 ; TYPE: DNA ; ORGANISM: Chlamydia pneumoniae ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)..(2808) US-10-324-129-2 | | | | |
| Query Match 15.9%; Score 477; DB 13; Length 2808; Best Local Similarity 51.4%; Pred. No. 1.8e-122; Matches 1451; Conservative 0; Mismatches 1300; Indels 74; Gaps 12; | | | | |
| | QY | 101 | ATGAAGTCTCTTTCCCCAAGTTGTATTTTCTACATTTGCTATTTTCCCTT---TGTC | 157 |
| | Db | 1 | ATGAAGTCTCTCTGCTCTCTGTTCTTTTCTCAATCCCGCTCTTTTCAATCGCTCTCT | 60 |
| | QY | 158 | ATGATGTCTACCGACAGAGTTTTCGATTCAG-- --TGGAGTTTCGATGGGAATAAAAAA | 214 |
| | Db | 61 | ATAGTCGGCAGAGGTCACCTTAGATAGCAATAATAGCTATGATGATCAACCGA | 120 |
| | QY | 215 | GGTAATTTTTCAGTTCGTGAGAGTCAGGAAGATGCT---GGAACTACCTACTATTTAAG | 271 |
| | Db | 121 | ACTACCTTCAGGCTCTTTTCCACTACGACGCTGCTGCAGAACTTACCTATTCCCTACTT | 180 |

QY 272 GGAAATGTCACCTCTAGAAAATTCCTCGAAGCAGCAATCAGAAAAGCTGTTT 331
DB 181 TCGGAGTATCTCTTCAAAATGCGGGCTTTAGGAATTCCTTAGCCTCAGGATGCTTC 240
QY 332 AACAAACATTAAGGGGATTTGACTTTTCAGGTAAACGGGAATCTCTATTGTTCCAAAGC 391
DB 241 CTAGAAGCGGGCGGATCTTACTTTTCCAGGAATCAACATGCACTGAAGTTGCAATT 300
QY 392 GTGGATGACGAGACTGTAGCAGGGGTGCTGTTTAAACAGCAGCGTGGTAGATAAATCTACC 451
DB 301 ATCAATGCGGGCTCTAGCGCTGGAATCTGAGCCAGTACTCAGCAGCAGATAAAGAACTCT 360
QY 452 ACGTTTATAGGGTTTCTTCGCTATCTTTTATGCGTCTCTCGGAAGTTCGATACTACC 511
DB 361 CTCCTTTAATGATTTTCTAGACTCTCTATATCTCTGTCCTCTCTCTCTCTCTCT 420
QY 512 GCAAGGAGCGGTAGCTGCTCTACGGGTAGCTTGAGTTTGACAAAAATGTCAGTTTG 571
DB 421 ACTGACAAATGCTTTAAATCTGTGGGAATCTATCTCTAACTGGCAATTCCTCAAAAT 480
QY 572 CTCCTCAGCAAAATCTTTCAACGGATAATGGCGGTGCTATCAACGCAAAAATCTTTCA 631
DB 481 ATATTTACTCGAATCTCTCGTCAATACCGCGGTGTTATCAATACGAAAAATCTCTTA 540
QY 632 TTAAACAGGACTACAATGTCAGCTCTGTTTCTGGAATATCCTCTCA-----AAGAAA 685
DB 541 TTATCAGGGAATCTCAGTTTGGAGCTTTTCGAAACCCAGGCTTCACAGGGGAAGCAA 600
QY 686 GCGGAGCCATTCAGACTTCGATGCCCTTACCAATTAAGTGAACCAAGGGGAAGTCTCT 745
DB 601 GCGGTGTAGTTTACGCTACAGGAATATACTATCGAGAACAGCCCTCGGATAGTTTCC 660
QY 746 TTTTCTGCAATATCTTTCGATCTCGAGTCTGCAATTTTTCAGAAAGCCTCGGTGACT 805
DB 661 TTCTCTCAAAACCTAGCGAAAGATCTGGCGGTGCTCTGTACAGCACTGACAATGTTTCG 720
QY 806 ATTTCTTAATATGCTTAAAGTTTCTTTTATTCAGATATAGTTCAGAGGCGAGCTCCTCA 865
DB 721 ATTAAGATAATCTTCAAGTGAATCTTTGACGGCAATAGTGTGGGAAGCGCTCAAGCT 780
QY 866 ACAACGGGGATATGTACAGGAGTGTCTATCTGTCTTATAAACTAGTACAGATACTAAG 925
DB 781 CAGGGCGGGCTAT-----TTGTTGCACTACGACAGATAAACA 819
QY 926 GTACCCCTCCTGMAATCAGATGTTACTCTTCAGCAACAATACATCGAACACGCGGA 985
DB 820 GTGACTCTTACTGGGAACAAAAACCTCTCTTTTCAAAATAATACAGCAATTCACATATGGC 879
QY 986 GGAGCTATCTATGTGAAAAAGCTCGAAGTGGCTTCGGGAGCACTTACCCTATTTCAGTAGA 1045
DB 880 GGAGCCATCTCTGACTCAAGGTGAGTATTTCCGCTGGAGTCTCTACTCTATTTTCAAGT 939
QY 1046 AATAGTGTCAAATGGAGGTACAGCTC---CTAAGGTGGAGCCATAGCTATTCGAAGATAGT 1102
DB 940 AATATCTCAGGAAGTAGCGCGGTACGGGAGGAGGAGCGATCAATATAGCATCTGCT 999
QY 1103 GGGGAATGAGTTTATCGGCGGATAGTGGTCAATTTGTTTATGGGAATPACAGTCACT 1162
DB 1000 GGGGAATCGCTCTCTCTGCTACTTCTGGAGATATTACCTTCAATAACAACCAAGTCACC 1059
QY 1163 TCTACTACTCTCGGAGCAATAGAGTAGTATCGACTTAGGAAGGAGTGCAGAGATGACA 1222
DB 1060 AACGGAAGCAAGATACAGAAACGCAATAAATATCATTTGATAC---CGCTAAAGTCA 1116
QY 1223 GCTTTGGCTTCTGCTGTGGTAGAGCCATCTACTTCTATGATCCCA-TAACTACAGGATC 1281
DB 1117 TCGATACGAGTCTACGGGCAATCTATCTATTTCTATGATCCCATTCACAAATCCAGG 1176
QY 1282 ATCCAAACAGTTACAGATGCTTTAAAGTTAATGAGACTCCGCGAGATTTGCACTACA 1341
DB 1177 AACCGCAGCTTCTACCGACACATTAAGTAACTTAACTTAGCAGATCGCAACAGTGAGATCGA 1236

QY 1342 ATATACAGGGAACATCATCTCTTCAAGGAGAAAAGTTATCAGAGACAGAGCGCGCAGATTC 1401
DB 1237 GTATGGGGTGCAGATTGTTCTTTCTGGAGAAAAGCTTTCCCTACAGAAAAAGCAATCGC 1296
QY 1402 TAAAAATCTTACTTTCGAAGCTACTACAGCCTGTAACTCTTTTCAGGAGGTACTCTATCTTT 1461
DB 1297 TGCAAAAGTCACTCTACTATCCGACAACTTCGAGTATTAGCGGGGAGATCTTTGTACT 1356
QY 1462 AAAACATGAGGTGACTCTGACAGACTCAGGCATTCCTCAACAGGCGAGATTCTCGTCTCGA 1521
DB 1357 TCGTATGGAGTCAACCGTAACTTTCAAGGATCTGACTCAAGTCCAGGATCCGCACTTT 1416
QY 1522 AATGACGTAGAACTACTCTAGAACCT---GCTGATACTAGCACTCAATAAATTTGGT 1578
DB 1417 AATGGATGGGAGGATACACTTAGTGTAAAGAGCAAACTTTTCGCTTAATGGCTTAGC 1476
QY 1579 CATTAAACATCAGTTCTATAGACGTCGAAAGAGGCAAAAATAGAACCAAGCTACGTC 1638
DB 1477 AGTAAATCTCTCTCTTTTAGATGGAACCAACAGGAGCTTTTAAAAACAGAACTGCAGA 1536
QY 1639 AAAAAATCTGACTTTATCTGGAACCATCATCTTTATGACCCGACGGGCGACGTTTATGA 1698
DB 1537 TAAAAATATCAGCCTATCGGGAACGATTGCGCTTTATTGACACGGAAGGTCAATCTATGA 1596
QY 1699 AAATCATAGTTTAAAGAAATCCTCAGTCTCTAGCACTCTTAGAGCTCA-----AAGC 1749
DB 1597 GAATCATAACTTAAAAAGTGTAGTACTCTCTCTTCTTGAACCTTACCACCGCAGGAGC 1656
QY 1750 TTCTGGAACCTGTAAACAGCAGCGAGTACTCCAGATCTTATATGGGGAGACGGGCTTCTACGACTGC 1809
DB 1657 CAACGGAACGATTACTCTGGAGCTCTTTTACCCCTGACTCTTCAAGAAACCTGAAACCCA 1716
QY 1810 TTACGGCTATCAGGAACTTTGGGGCCCAATTTGTTGGGGAGACGGGCTTCTACGACTGC 1869
DB 1717 CTACGGGTACAAGGAACCTGSCAGTGTCTTGGGCAATG-CAACATCTCTCAAAAATAGG 1775
QY 1870 AACCTTCAACTGGAATAAACTGCTATATTTCTTAATCCGAGGATATCGGCTCTTTAGT 1929
DB 1776 AAGCATCAACTGGACCGGTACAGGATACATTCCTTAGTCTTGAGAGAAAAAGTAATCTCCC 1835
QY 1930 CCCTTAATAGCTTATGGAATGCATTTATAGATATAGCTCTCTCCATTTCTTATGGAGAC 1989
DB 1836 TCTAATAGCTTATGGGGAACCTTTATAGATATACGCTCGATCAATCAGCTTATAGAAAC 1895
QY 1990 TCGAAACGAAGGTTGACGGGAGACCGGTGTTTTGTTGTTGCTGATTAATCTAATCTCT 2049
DB 1896 CAAGTCCAGTGGGAGCCTTTTGAGCGTGAGCTATGCTTTCAGGAATTCGGAATTTCTT 1955
QY 2050 CCATAAGGATAGTACAAAAACAACGACGGGTTTCGCAATTTGAGTGGCGGTTATGTCAT 2109
DB 1956 CTATAGAGATTCTATGCCCCACCGCCATGTTTTCGCCATATCAGCGGGGTTATGCACT 2015
QY 2110 AGGAGGAAACCTACATACTTTGTCAGATAAGATTTCTTAGTCTGCAATTTTGTGAGCTCTT 2169
DB 2016 AGGATCACAGCAACAACCTCTCGGAGGATCAGCTTACTTTTTGCTCTCTGCGAGCTCTT 2075
QY 2170 TGAAGAGATAGAGACTACTTTGAGCTAAGAAATCAAGGTACAGTCTAACGAGGAACTCT 2229
DB 2076 TGCTAGAGATCGCAATCATATTACAGTAAAGAACCAAGGATACTTACGGTGCCTCTTT 2135
QY 2230 CTATTACCAGC-----ACAACGAACCTATATCTCTCTCTCTCTCTCTCTCT 2271
DB 2136 GTATTTCCACCATACAGAAGGCTCTTTCGACATCGCAATTTCTCTGGGAAAAAGCAAC 2195
QY 2272 ACTACGCGCTTGTTCGTTGTTCTTATGTTCTCCTACAGATTTCTGTTCTCTTTTCAGAAA 2331
DB 2196 CCGAGCTCCCTGGTGTCTCTGAGATCTCCAGATCATCTCTTTATCGTTGATGCTAA 2255
QY 2332 CCTTAGCTACACCCATACGGAATACGATCTGAAAAACCAAGTATACACATATCTCTACTGT 2391
DB 2256 ATTCAGTTATCTCCATACAGAACCAACATGAAGACATATTATACGATAACTCTATCAT 2315
QY 2392 TAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGAAGAGCTCCGATTG 2451

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Db 2316 CAAGGCTTCTGGAGAAAGATCCCTTCTGTGCAGATCTTGGAGCTAGCCTTGTGT 2375
QY 2452 CTTAGATGAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTCAGATTTGTCTA 2511
Db 2376 TATTTCCGTTCCGTAACCTTCTGAAGAAGTTCGAACCTTTTGTCAAAGTACAGTATATCTA 2435
QY 2512 TGCACATCAGGAGGTTTAAAGAAACAGGAACAGAGCTCGTGAATTTGGAAGTAGCGG 2571
Db 2436 TCGGCATCAGCAAGACTTCTACAGAGCTCATGTGAAGGACGCGCTTTCAATAAAGCGA 2495
QY 2572 TCTTGTGAATCTTGCTTACTTATCGGATCCGATTTGATTAAGGAATCAGACTGCCAAG 2631
Db 2496 GCTTATCAAGCTAGAGATTCCTATAGCGTCACCTTCGAAGAGACTCAAAATCAGAAA 2555
QY 2632 TGAACGTACAATCTAACTCTTGTTATATCTGTGATCTTGTTCGTAGTAACCCGACTG 2691
Db 2556 GGGAACTTACGATCTTACTCTTATGATATATCTCGATGCTTACCGACGCAATCCTAAATG 2615
QY 2692 TACGACACACTCGAATTAGCGGTGATCTTGGAAAACTTCGGTACGAATTTGGCAAG 2751
Db 2616 TCAAACTTCCCTAATAGTAGCGATGCTAACTGGATGGGCTATGTACCAACCTCGCACG 2675
QY 2752 ACAAGCTTTAGTCTCTGTCAGGGAACCAATTTTTCCTTTAACTCAAAATTTTGAAGCCTT 2811
Db 2676 ACNAGGTTTTCTGTTGCTGCTCGAACCAATTTCCAGTGAACCCCAATGGAATCTT 2735
QY 2812 TAGCCAAATTTCTTTGAATTCGTTGGTCACTCGCAATCAATGTAGACTTAGAGC 2871
Db 2736 CGGTCAATTCGCTTTTGAAGTACGAAGTCTTCCAGGAATTAATAACAAACCTAGGCTC 2795
QY 2872 AAAAT 2876
Db 2796 TAAAT 2800

RESULT 8
US-09-738-269-22
; Sequence 22, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEWKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; FILE OF INVENTION: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738, 269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-22

Query Match 11.6%; Score 348.4; DB 13; Length 2520;
Best Local Similarity 50.6%; Pred. No. 2.1e-86;
Matches 1101; Conservative 0; Mismatches 1006; Indels 69; Gaps 8;

QY 760 TTTCTCGATCTGGAGCTGCAATTTTACAGAGGCTCGGTGACTATTCTTAATAATGC 819
Db 366 TTCTTTATTTTCATGTGCTATTGTCTCCAGGACAACTGGTTACGGAGCTATACAGAC 425
QY 820 TAAAGTTCTTTTATGACAAATAGGTCACAGAGGAGGCTCTCAACACGGGGGATAT 879
Db 426 TAAAGGCAACACAACTTTAAAGATAACTCTAGTCTTGTCTTCCATAAAACTGTCTCAAC 485
QY 880 GTCAGGAGGTGCTATCTGTCTTATAAACTAGTACAGATCTAAGGTCACCCCTCACTGG 939
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Db 486 AGCAGAAGGTGGGGCTATCCAGTGTAAAGGAAGCAGTGTCTGATTTAAAAATAGAAA 545
QY 940 AAATCAGATGTTTACTCTTTAGCAACAATACATCGAACAAGCGGGAGGAGCTATCTATGT 999
Db 546 TAATCAGAATCTGGTTTCTCAGAAAACCTCTCCACTTCAAAAAGCGGGGCTATTATGTC 605
QY 1000 GAAAAGCTCGAATCGGCTTCCGGAGGACTTACCCCTATTACGTAGAAAATAGTGTCAATGG 1059
Db 606 TGATAAACTCACCATTTGTCTCAGGTGGGCTTACATTTATTTCTTAAACAATCTGTATCAAA 665
QY 1060 AGGTACAGCTCCCTAAAGGTGGAGCCATAGCTATCAAGAT---AGTGGGAATTCAGTTT 1116
Db 666 CGTTTCATCCCTTAAAGCGGAGCTTTAGCATAAAGATTCAGTGGTGAATGTAGCCT 725
QY 1117 ATCCGCGATAGTGTGACATTTCTTTTAAAGGAATACAGTCACTTTCTACTACTCTGG 1176
Db 726 AACCGCTGATCTCGAGATATTACCTCGATGGGAACAAATCATCAAAACTAGTGGTGG 785
QY 1177 GACGAATAGAGTATTCGACTTAGGAACG-----AGTGCAAGATGACAGCTTTGGG 1230
Db 786 AAGTTCTACAGTAAACAAGAAATTCATAGATCTCGGCACAGGAAATTTACAAAGCTAGC 845
QY 1231 TTCTGCTGTGTAGAGCCATCTACTTCTATGATCCCATACTACAGGATCATCCACAAC 1290
Db 846 TGTAAAGACGGCTTCGGNAATTTCTTATGACCTTATTACTGGGGAGGATCTGATGA 905
QY 1291 AGTTACAGATGCTTAAAGTTTAATGAGACTCCGCGAGATTTCTGCACACTACATATACAGG 1350
Db 906 ACTAAACATTAATAAAAAAGAACTG-----TTGATTATACAGG 944
QY 1351 GAACATCATCTTCAGAGGAAAGTTATCAGAGACAGAGCCGCGAGATTTCAAAAATCT 1410
Db 945 AAGATCGTCTTCTCAGGTGAAAAATTTATCGATGAAGAAAAGCAGAGCGGAAAACT 1004
QY 1411 TACTTCGAAGTACTACAGCTGTAACTTTTTCAGAGGAGTACTCTATCTTTAAAAACATGG 1470
Db 1005 AGCTTCTACTTTCAACCAACCCATCACATTATCAGCAGGATCTCTTGTACTTTAAGATGG 1064
QY 1471 AGTGACTCTGAGACTCAGGCAATTCCTCAACAGCAGATTTCTGTCTCGAATAAGACT 1530
Db 1065 TGTATCTGTAAACCGCAAAACAAGTAACGAGGAAGCGGATCTACCGTTGTCTATGGATCT 1124
QY 1531 AGGAATCTACTAGAACCTGCT-----GATACTAGCACCATAAACAATTTGGT 1578
Db 1125 AGGGACCACTTACAGACGCTTCTTCAGGTGGAGAAACCATCACCTAACTAATCTAGA 1184
QY 1579 CATTAACATCAGTCTTATAGACGCTGCAAGAAAGCAAAAATAGAAA-----CCAAAGC 1632
Db 1185 TATTAACTCGCTCGTTGGGGGGGGGGGTACTCTCTGCTTAACTCGCAACAA 1244
QY 1633 TAGGTCAAAAAATCTGACTTTTATCTGGAAACCATCACTTTTATGGACCCGACGGCACTG 1692
Db 1245 TACAGCAAGTCAAGCTATAAATCTATTAAACGCTCAATCTAGTCGATGCTGATGGCAATGC 1304
QY 1693 TTATGAATATCATAGTTTAAAGAAATCCCTCAGTCTTACGACATCTTAGAGCTCAAGCTTC 1752
Db 1305 TTATGAAGATCTCTATTCTTGTACTCTTAAACCTTTACAGCAATAGTAGTACAACTAA 1364
QY 1753 TGGAACTGTAAACAAGCACCGCAGTCTGACTCCAGATCTTAAATGGGTGAGAAATTCATTA 1812
Db 1365 CGCTAGTACAGTCAACAGCCTACAGATAATCTAACAAATATATGTCCCTCTACTCATTA 1424
QY 1813 CGGCTATACGGGAACTTGGGGCCCAATTTTGGGGGACAGGGGCTTTTACGACTGCAAC 1872
Db 1425 CGGTTACCAAGAAATTTGACAGTAACCTTGGGACACCCGAAACAGCTACAAAAACAGCCAC 1484
QY 1873 CTTCAACTGGACTAAACTGGCTATATTCTTAACTCCGAGCGTATCGGCTCTTTAGTCC 1932
Db 1485 TCTAACTTTGGGAAACAACTGGCTACTCCCTTAACCCAGAACGCTCAAGGACCTTTAGTCC 1544
QY 1933 TAAATAGCTTATGGAATGCAATTTATAGATATTAGTCTCTCCATTTATCTTATGGAGCTGC 1992
Db 1545 GAATACTCTTTGGGTGCAATTTCTGACCTCAGAGCTTATACAAAACCTTAATGGATATTAG 1604
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1993 AAAAGAGGTTGACGAGACCGTGCTTTTGGTGTGCTGGATTATCTAACTTCTTCCA 2052
Db CGTCAATGGCGTGACTACCATAGAGGTTTTTGGGTATCCGGTCTAGCTAACTTCTTACA 1664
2053 TAAGGATAGTACAAAACACAGACGGGTTTCGCCATTAGTGGCGGTATGTATAGG 2112
Db CAAAAGTGGCTCTGATACCTAAAGCAAGTTCGGTCAATAGCGCGGATACGCTTTAGG 1724
2113 AGAAACCTACATCTTGTTCAGATAAGATTCTTAGTGTGCTGCAATTTGTAGCTCTTTGG 2172
Db CGTCTACGCAAAACCTCTCTGATGATATTTTCACTGGCGGCTTCTGCCAATCTTCGG 1784
2173 AAGAGATAGAGACTTTTGTAGCTTAAGATCAAGGTACAGTCTACGGAGGAACTCTCTA 2232
Db AAAGCAAAAGACTATTTAGTGTGCAAAACCAACGCCAATTTACGCAAGTTCTCTCTA 1844
2233 TTACGAGCACACGAAACCTATATCTCTCTTCTTGCACAACTACGGCCTTGTCTGTCTC 2292
Db TTATCAGCATATCTCTATTTGGAGCGCTTGGCAGATCTGCTACAAACACTATCGGTGC 1904
2293 TTAGTTCCTACAGAGATTCCTGTCTCTTTTCAGGAAACCTTAGCTACCCATACGGA 2352
Db AGAAGCTCGGTAGTCTTAAAGCACAGTAACTTAATGTGTCATGCTTCAAACGACATGAA 1964
2353 TAAAGATCTGAAACCAAGTAT-----ACACATATCTTACTGTTTAAAGGAAG 2400
Db AACCAATAGCAGTACTTACGCTCTCGTAAACCAACGATGAGAAATCAAGGGTGA 2024
2401 CTGGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGAAGAGCTCCGATTTGCTTAGATGA 2460
Db TTGGGTAACGATTTTTCGGAGTCGAGCTTGGTGCACTGTGCTATCCAAACAGATC 2084
2461 AAGTCTCTATTTAGCAGTACATGCCCTTCAATGAATTCAGATTTGTCTATGACATCA 2520
Db TTCTCTCTATTCGATATGTACTCACCTTTCTGAAATTTCAACTTTGTCATACGCCA 2144
2521 GGAAGGTTTTAAAGAACAGGGAACAGAA--GCTCGTGAATTTGGAAGTAGCCGCTTGT 2577
Db AGATGACTTTAAGGAAACATAGCGATCAGGGAAGATCTTTGAAAGCAGCAATCTCAC 2204
2578 GAATCTTGCCTTACTATCGGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAAC 2637
Db CAACCTTCTCTGCTATCGCATCAAGTTTGAGGATTTGCTACACAGATACAGCTTC 2264
2638 GTACATCTAATCTTGTGTTATATGNGGATCTTGTTCGTAGTAAACCCGACTGTACGAC 2697
Db TTATCATGCTACTGCTGCTTATCTCTGATATCGTAAAGAGTAAACCCGACTGTACTAC 2324
2698 AACACTGGAATTTAGCGGTGATCT-----TGGAACCTTCGTAGCAATTTGGCAAG 2751
Db TTCTCTGTAGTAAACCCGACTCTGCTGCTGGGTAAAGAACCAACACCTTTGGCGG 2384
2752 ACAAGCTTTAGTCTCTCGTCAGGGAACCAATTTTGTCTTTAACTCAAAATTTGAAGCCTT 2811
Db AAGGCTTCTCATGTACAAAGCAGGAAACTACTTGTCTTTAGTACACATAGAAATCTT 2444
2812 TAGCAATTTCTTTGAAATGCGTGGGTATCTCGCAATTTCAATGTAGACTTAGGAGC 2871
Db CAGCGAGTTCGGTTTCAGCTCAGGGGATCTTCAAGAACCTTAAACGTAGATCTCGGATC 2504
2872 AAAATACCAATTTCTAA 2887
Db GAAGATCCAGTTCTAA 2520

RESULT 9

US-10-023-437-22

; Sequence 22, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE

; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACI
; FILE REFERENCE: US/10/023,437
; CURRENT APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-10-023-437-22

Query Match 11.6%; Score 348.4; DB 14; Length 2520;
Best Local Similarity 50.6%; Pred. No. 2.1e-86;
Matches 1101; Conservative 0; Mismatches 1006; Indels 69; Gaps 8;
QY 760 TTCTTCGGATTCTCGAGCTGCAATTTTACAGAAAGCCTCGGTGACTATTTCTTAATAATGC 819
Db 366 TTCTTTATTTTCATGTGCTTATTGCTCTCCAGGCACAACTGGTTACGGAGCTATACAGC 425
QY 920 TAAAGTTTCCTTTTATGACATAAGGTCAACAGGACGAGTCTCTCAACACGGGGATAT 879
Db 426 TAAAGCAACACAACTTTTAAAGATAAATCTAGTCTTGTCTTCCATAAAACCTGCTCAAC 485
QY 880 GTACAGGAGTCTATCTGTGCTTATAAACTAGTACAGATACTAAGTCAACCTCCTCTG 939
Db 486 AGCAGAGGTGGGCTATCCAGTGTAAAGAGCAGTGTGCTGAATTTAAATAATAGAAAA 545
QY 940 AAATCAGATGTTACTCTTTCAGCAACAATATATCGCAACACAGCGGAGGAGCTATCTATGT 999
Db 546 TAATCAGAACTCTGTTTCTCAGAAACTCTCTCACTTCAAAAGCGGGCTATTATGCG 605
QY 1000 GAAAAAGCTGCACTGGCTTCGGAGGACTTACCTATTCAGTAGAATAAGTGTCAATGG 1059
Db 606 TGAATAAATCACCATTGCTCTCAGGTGGGCTTACATTTATTTCTAACAACTCTGTATCCNA 665
QY 1060 AGGTACAGCTCTTAAAGGTGGAGCCATAGCTATCGAAGAT---AGTGGGAATTTAGTTT 1116
Db 666 CGGTTCTATCCCTTAAAGCGGAGCTATTAGCATAAAGATTTCAAGTGGTGAATAGCCT 725
QY 1117 ATCCGCGATAGTGGTGACATTTGCTTTTAGGGAATACAGTCACTTCTACTCTCTCTGG 1176
Db 726 AACGCTGATCTCGAGATATTACCTTCGATGGGAACAAATCATCAAACTAGTGGTG 785
QY 1177 GACGAATAGAGTAGTATCGACTTAGGAACG-----AGTCAAGATGACAGCTTTGCG 1230
Db 786 AAGTTCTACAGTAAACAGAAATTCATAGATCTCGGCACAGGAAATTTACAAAGTACG 845
QY 1231 TTCTGCTGCTGGTAGAGCCATCTACTTCTATGATCCCACTACAGATCATCCACAC 1290
Db 846 TGCTAAAGACGGCTTCGAAATTTTCTTATGACCTTATTACTGGGGAGGATCTGTAGA 905
QY 1291 AGTTTACAGATGTCTTAAAGTTAATGAGACTCCGCGAGATTTCTGCACATAAATATACGG 1350
Db 906 ACTAAACATTAATAAAGAACTG-----TTGATTAATACAGG 944
QY 1351 GAACATCATCTTCAAGGAGAAAGTTATCAGAGACAGAGCCGCGAGATTTCTAAAAATCT 1410
Db 945 AAAGATCGTCTTCTCAGGTGAAAAATTTATCCGATGAAGAAAAAGCAGCGAGGAAACCT 1004
QY 1411 TACTTCGAAGCTACTACAGCTGTACTCTTTTTCAGGAGGTACTCTATCTTTTAAACATGG 1470
Db 1005 AGCTTCTACTTTCAACCAACCATCATATCAGCAGGATCTCTTGTACTTAAAGATGG 1064
QY 1471 AGTGACTCTGCAGACTCAGGCATTTCACTCAACAGGAGATTTCTCGTCTCCAAATGGACGT 1530
Db 1065 TGTATCTGTAAACCGCAAAACAAAGTAAAGCAGGAGGAGTCTACCGTTGTCTATGATCT 1124

| | | | |
|----|------|---|------|
| Qy | 1531 | AGNACTACTCTTAGAACCTGCT-----GATACTAGCACCATTAACAAATTTGGT | 1576 |
| Db | 1125 | AGGGACACAAATTACAGACGCCTTCTTTAGGTGAGAAACCATCACCCCTAACTAATCTAGA | 1184 |
| Qy | 1579 | CATTACATCAGTTCTATAGACCGTGCAAAGAGGCAAAATAGAA-----CCTAAGC | 1632 |
| Db | 1185 | TATTAAACATCGCTCGTTGGGGGGGGGGGGGTACCTCTCTGCTTAAACTCGCAACAA | 1244 |
| Qy | 1633 | TAGCTCAAAAATACTTGACTTTTATCTGGAAACCATCACTTTATTGGACCCGACGGCAGCTT | 1692 |
| Db | 1245 | TACAGCAAGTCAAGCTATTAACCTATTAAACGCTGTCAATCTAGTCGATCTGATGCGAATGC | 1304 |
| Qy | 1693 | TTATGAAATCATAGTTTAAAGAAATCCTCAGTCTCTAGCAATCTTAGAGCTCAAAAGCTTC | 1752 |
| Db | 1305 | TTATGAAGATCCTATTCTTGCTACGCTTAAACCTTTTACAGCAATAGTAGTACAACTAA | 1364 |
| Qy | 1753 | TGGNACTGTTAACAGCACCCGAGTGACTCCAGATCTCTATTAATCGGTGAGAAATCCCATTA | 1812 |
| Db | 1365 | CGCTAGTACAGTACACAGCCCTACAGATAATCTAAACAAATATGTCCCTCCTACTCATTTA | 1424 |
| Qy | 1813 | CGGCTATCAGGGAACCTTGGGGGCCCAATGTTTGGGGACAGAGGGCTTCTACGACTGCAAC | 1872 |
| Db | 1425 | CGGTTACCAAGGAAATGGACAGTAACTTGGGACACCGAAACAGCTACAAAACAGCCAC | 1484 |
| Qy | 1873 | CTTCAACTGGACTAAAACTGGCTATATTCCTAATTCGAGCGGTATCGGCTCTTTAGTCCC | 1932 |
| Db | 1485 | TCTAACTTGGGAACAAACTGGCTACTCCCTTAACCCAGAAAGCTCAAGAGACCTTTAGTCCC | 1544 |
| Qy | 1933 | TAAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCTCCATTTATCTTAATGAGACTGC | 1992 |
| Db | 1545 | GAATACTCTTTGGGGTGCAATCTCTGACCTCAGAGCTATACAAACTTTAATGATATTAG | 1604 |
| Qy | 1993 | AAACGAAGGGTTGCAGGAGACCGTGCTTTTGGTGTGCTGGATTAATCTAACTTCTTCCA | 2052 |
| Db | 1605 | CGTCAATGGCGCTCACTACCATAGAGGTTTTGGGTATCGGCTAGCTAACTTCTTACA | 1664 |
| Qy | 2053 | TAAGGATAGTACAAAAACAGACGCGGGTTTCGCCATTTGAGTGGCGGTTATGTCTATAGG | 2112 |
| Db | 1665 | CAAAAGTGGCTCTGATACTAAACGCAAGTTCCGCTCACAATAGCGCCGGATACGCTTTAGG | 1724 |
| Qy | 2113 | AGGNAACCTACATCTTTGTCAGATAGATCTTAGTGTCTGCAATTTTGTGAGCTCTTTGG | 2172 |
| Db | 1725 | CGTCTACGCAAAAACCTCCTCTGTATGATATTTTCAGTGGCGGCTTTTCGCAACTCTTCGG | 1784 |
| Qy | 2173 | AAGAGATAGAGACTTACTTTGTAGCTAAGAACTCAAGTCAAGTCTACGGAGGAATCTCTTA | 2232 |
| Db | 1785 | AAAGGACAAAGACTATTTAGTGTGCAAAACACGCCAAATTTACGAGGTTCTCTCTTA | 1844 |
| Qy | 2233 | TTACGAGCAACGAAACCTTATATCTCTCTCTCTTTCGAAACTACGGCGCTTGTGCTGTGC | 2292 |
| Db | 1845 | TTATCAGCATATCTCCTATTGGAGCGCTTGGCAGAACTGTCTACAAAACACTATCGGTGC | 1904 |
| Qy | 2293 | TTATGTTCTTACAGAGATTCTGTGTTCTTTTTCAGGAAACCTTAGCTACACCCATACGGA | 2352 |
| Db | 1905 | AGAAGCTCCGTTAGTCTCTTAACGCACAGTTAACTTTATGTGATGCTTTCAAACGACATGAA | 1964 |
| Qy | 2353 | TAAAGATCTGAAAAACCAAGTAT-----ACAACATATCCTACTGTTTAAAGGAAG | 2400 |
| Db | 1965 | AACCAACATGACGACTACTTACGCTCCTCGTAAACAAACGATGACAGAAATCAAGGTGA | 2024 |
| Qy | 2401 | CTGGGGGAATGATAGTTTCGCTTTTAGAATTCGGTGGAGAGCTCCGATTTGCTTTAGATGA | 2460 |
| Db | 2025 | TTGGGGTAACGATTGTTTCGGAGTCGAGCTTGGTGCAACTGTGCTATCCAAAACAGAAATC | 2084 |
| Qy | 2461 | AAGTGCTCTATTTGAGCAGTATACGCCCTTCATGAATTCAGTTTGTCTATGACATCA | 2520 |
| Db | 2085 | TTCTCTCCTATTCGATATGTACTCACCTTCTCCTGAAGTTTCAAGCTTGTGCATAGCACCA | 2144 |
| Qy | 2521 | GGAAAGTTTTAAAGAACAGGGAACAGAA--GCTCGTGAATTTTGGAAAGTAGCCGCTTGT | 2577 |
| Db | 2145 | AGATGACTTTTAAAGAAACAAATAGGATCAGGGAAGATATCTTGGAAAGCAGCAATCTCAC | 2204 |
| Qy | 2578 | GAATCTTTCCTTATCCTATPCGGGATCCGATTTTGATAAGGAATCAGACTGCCAAGTAGCAAC | 2637 |

| | | | |
|------|----|---|------|
| 2205 | Db | CAACCTTTCTCGCTATCGGCATCAAGTTTGAGAGATTGCTAACACGATACAGCTTC | 2264 |
| 2638 | Qy | GTACAACTCAACTCTTGGTTATACTGTGGATCTTGTTCGTAGTAACCCCGACTGTACGAC | 2697 |
| 2265 | Db | TTATCATGTCACCTGCTGCTATTCTCTCTGATATCGTAAGAAGTAAACCTGACTGTACTAC | 2324 |
| 2698 | Qy | AACACTGCGAATTAGCGGTGAATCT-----TGGAAACCTTCGGTAGCAATTGGCAAG | 2751 |
| 2325 | Db | TTCTCTGTTAGTAAGCCCGCACTCTGCTGTGGGTAAACGAAACCAACCTTGGCG | 2384 |
| 2752 | Qy | ACAAGCTTTAGTCCTTCGTACGAGGACCATTTTGTCTTTAACTCAAAATTTGAGGCTT | 2811 |
| 2385 | Db | AAGCGCCTTCATGCTACAACGAGAAACTACTTGTCTTTAAGTCACAACTAGAAATCTT | 2444 |
| 2812 | Qy | TAGCCAAATTTCTTTTGAATTCGGTGGTCATCTCGCAATTACAATGTAGACTTTAGGAGC | 2871 |
| 2445 | Db | CAGCCAGTTCGGTTTCGAGCTCAGGGATCTTCAACGACCTATAACGTAGATCTCGATC | 2504 |
| 2872 | Qy | AAATACCAATTTCTAA | 2887 |
| 2505 | Db | GAAGATCCAGTTCTAA | 2520 |

RESULT 10
 US-09-886-468-6
 ; Sequence 6, Application US/09886468
 ; Patent No. US20020037293A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aventis Pasteur Limited
 ; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses the
 ; FILE REFERENCE: 77813-5
 ; CURRENT APPLICATION NUMBER: US/09/886,468
 ; CURRENT FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: 60/113,280
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/113,281
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/113,282
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/113,283
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/113,284
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/113,285
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/113,385
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/114,050
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: 60/114,056
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: 60/114,057
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: 60/114,058
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: 60/114,059
 ; PRIOR FILING DATE: 1998-12-28
 ; PRIOR APPLICATION NUMBER: 60/114,061
 ; PRIOR FILING DATE: 1998-12-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 2950
 ; TYPE: DNA
 ; ORGANISM: Chlamydia pneumoniae
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (101)..(2866)
 US-09-886-468-6

| | | | | |
|-----------------------|--------|--------------------|-------|--------------|
| Query Match | 9.1%; | Score 271.8; | DB 9; | Length 2950; |
| Best Local Similarity | 48.0%; | Pred. No. 7.5e-65; | | |

| | | |
|---|------|---|
| Matches 1351; Conservative 0; Mismatches 1362; Indels 102; Gaps 16; | | |
| QY | 122 | TTTGTATTTTCTACATTTTGTCTATTTTCCCTTTTGTCTATGTTGCTACCGAGACAGTTTGG 181 |
| Db | 134 | TTTTCCTTTTACATTTCTCAGTCTTCGACACTTCTTTGAGTGCTACTACGATTTCTTTTA 193 |
| QY | 182 | GATTCAGTGGCGATTTTCGATGGGAATAAATGTAATTTTTCAGTTTCGTGAGAGTCAG 241 |
| Db | 194 | ACCCAGAGAAGTAGTTTTCATGG-----AGATAGTCAGAATGCGAGAAGCTTTCTTATAAT 247 |
| QY | 242 | GAAGATGCTGGAACCTACCTACCTATTAAAGGGAATGTCACCTCTAGAAAATATTCTCTGGA 301 |
| Db | 248 | GTTCAAGCTGGGATGCTCTATAGCCTTACTGTGATGTCATATATCTAACTCGAT--- 304 |
| QY | 302 | ACAGGCAAGCAATCACAAAAGCTGTTTTTAAACAACCTAAGGGCGATTTGACTTTTACA 361 |
| Db | 305 | ---AACTCTGCTATTAAATAAAGCCTGCTCAATGTGACCTCAGGAAGTGTGACGTTGCGCA 361 |
| QY | 362 | GGTAACGGGAACCTCTATTGTTCCAAACGGTGGATCAGGGAAGTGA---GCAGGGCT 418 |
| Db | 362 | GGAAATCATATGCGTTTATATTTTAAATAATTTCTCTCAGGAACCTACAAAGGAAGGGCT 421 |
| QY | 419 | GCTGTAAACAGCAGCGTGTGTAGATAAATCTACCAAGTTTATAGGCTTTTCTTCGCTATCT 478 |
| Db | 422 | GTACTTTTGTGCAAGATCCTCAAGCAACGGCACGTTTTTCTGGGTTCTCCACGCTCTCT 481 |
| QY | 479 | TTTATTTGCGTCTCTGGAAGTTCGATAACTACCGGCAAGGAGCGGTTAGTGTCTCTACG 538 |
| Db | 482 | TTTATTCAGAGCCCGGAGATATTAA-----GAACAGGGATGTCTCTATTCAAAA 532 |
| QY | 539 | GGTAGCTTGAGTTTGACAAAATAATGTCAGTTTGTCTTTCAGCAAAAACCTTTTCAACGGAT 598 |
| Db | 533 | AATGCACCTATGCTCTTAAACAATTTATGTAGTGGCTTTTGAACAAAACCAAGTAAGACT 592 |
| QY | 599 | AATGCGGTGTCTATCACCGCAAAAACCTCTTTCAATTAACAGGGACTACAAATGTCAGCTCTG 658 |
| Db | 593 | AAAGCGGAGCTATTAGTGGGCGAATGTACTATATAGTAGCAACTACGATTCGCTCTCT 652 |
| QY | 659 | TTTTCTGAAAATACCTCTCAAGAAAAGCGGAGCCATTCAGACTTCGCGATGCCCTTACC 718 |
| Db | 653 | TTCTATCAGAATGCAGCC---ACTTTTGAGGTGCTATCCATTCTTCAGGTCCCTACAG 709 |
| QY | 719 | ATTACTGGAACCAAGGGGAGTCTCTTTTCTGACAATACTTCTCG---GATTTCTGGA 775 |
| Db | 710 | ATTGCAGTAAATCAGGCGAGATAGAATTTGCACAAAATACTGCCAAGAATGGTTCTGGA 769 |
| QY | 776 | GCTGCAATTTTACAGAAGCCTCGTGACTATTTCTAATAATGCTAAAGTTTCTCTTTATT 835 |
| Db | 770 | GGGGCTTTGTACTCCGATGGTGATATGATATTTGATCAGATGCTTATGTTCTATTTCGA 829 |
| QY | 836 | GACATAAGGTCACAGGAGCGAGTCTCTCAACAAACGGGGGATATGTCAGGAGGTGCTATC 895 |
| Db | 830 | GAAAATGAGG---CATTTGACTACTGCTATAGTAAGGAGGGGCTGTCTGTGTCTTCCC 886 |
| QY | 896 | TGTGCTTATAAACTAGTACAGATACTAAGTCAACCTCCTCAGTGGAAATCAGATGTTACTC 955 |
| Db | 887 | ACTTCAGGAAGTAGTACTCCAGTTCCTATTGTGACTTTTCTCTGACAATAAACAAGTTAGTC 946 |
| QY | 956 | TTTCAGCAACATATACATCGACAAACAGCGGAGAGTATCTATGTCAAAAAGCTCGAACTG 1015 |
| Db | 947 | TTTGAAGAAACCATTCATATATGGGTGGGAGGCCATTTATGCTAGGAACCTTAGCATC 1006 |
| QY | 1016 | GCTCCGGAGGACTTACCCTATTTCTAGTAGAATAGTGTCAATGGAGGTACAGCTCCTAAA 1075 |
| Db | 1007 | TCTTCAGGAGGTCCTACTCTATTATCAATAATATCATATGATCAAAATTCGCARAAATTA 1066 |
| QY | 1076 | GGTGAGCCATAGCTATCGAAGATAGTGGGAATTTGAGTTTATCCCGCGATAGTGGTAC 1135 |
| Db | 1067 | GGTGAGCTATTGCCATTGATCTGGAGGGGAGATCAGTTTATCAGCAGAGAAAAGAAACA 1126 |
| QY | 1136 | ATTGCTTTTATAGGGAATACAGTCACTTCTACTACTCTGGGACGAATAGAGTAGTATC 1195 |
| Db | 1127 | ATTACATTCAGGAA-----CCGGACGAGCTTACCCTTTTGAATGGCATC 1174 |

| | | |
|----|------|---|
| QY | 1196 | GACTTAGGAACGAGTGCAGGAAGATGACAGCTTTTGGCTTCTGCTGTGTAGAGCCATCTAC 1255 |
| Db | 1175 | CATCTTTTACAAAATGCTAAATTTCTGAAATTCACAGGCGAGAAATGGATACTCTATAGAA 1234 |
| QY | 1256 | TTCTATGATCCCATAACTACAGGATCATCCAAACAGTTACAGATGCTTTAAAAGTTAAT 1315 |
| Db | 1235 | TTTATGATCTCTATTACTTCTGAAGCAGATGGGTCTACCCAAATGAATATCAACGGAGAT 1294 |
| QY | 1316 | GAGACTCCGGCAGATTTCTGACTACAATATACAGGAACATCATCTTCACAGGAGAAAG 1375 |
| Db | 1295 | CCTAAAATAAAGAG-----TACACAGGACCATCTCTTTTCTGGAGAAAAG 1342 |
| QY | 1376 | TTATCAGAGACAGAGCGCGAGATTTCTAAAATCTTACTTCGAAGCTACTACAGCCTGTA 1435 |
| Db | 1343 | AGTCTAGCAACGATCTCTAGGATTTTAAA-----TCTACAAATCCCTCAGAACGTC 1393 |
| QY | 1436 | ACTCTTTACAGAGGTACTCTATCTTTTAAAACATGGAGTGACTTCGACAGCTCAGGCATTC 1495 |
| Db | 1394 | AACCTGTCTGCAGGATACTTTAGTTTATTAAAGAGGGGCGGAAGTCACAGTTTCAAAATTC 1453 |
| QY | 1496 | ACTCAACAGGCGAGATTTCTGCTCTCGAAATGACGTAGGAACCTACTCTAGAACCTGCT--- 1552 |
| Db | 1454 | ACGAGCTCTCAGGATCGCATTTTAGTTTAGATTTTAGGAACAAACTGATAGCCTCTAAG 1513 |
| QY | 1553 | ---GATACTAGCACCATAAACAATTTTGTCTAATTAACATCAGTTCTTATAGACGGTGCAAG 1609 |
| Db | 1514 | GAAGACATTTGCCATCACAGGCTCGCGATAGATATAGATAGCTTTAAGCTCATCTCTCAACA 1573 |
| QY | 1610 | AAGCAAAAATAGAAAACCAAGCTACGTCAAAATCTGACTTTTCTGGAACCATCACT 1669 |
| Db | 1574 | GCAGCTGTATTAAAGCAAAACACCGCAAAATAACAGATATCCGTGACGGACTCTATAGAA 1633 |
| QY | 1670 | TTATTGACCCGACGGGCACCGTTTATGAAAATCATAGTTTAAAGAAATCTCAGTCCCTAC 1729 |
| Db | 1634 | CTTATCTGCCCTACTCGGCAATGCCATTTAGAGATCTCAGATGAGAAATTCACAGAGTTC 1693 |
| QY | 1730 | GACATCTTAGAGCTCAAAAGCTTCTGAACTGTAAACAACCGCAGTGACTCCAGATCCT 1789 |
| Db | 1694 | CCTCTGCTCTCTTT---AGAGCTTGGAGCGGGGTAGTGTGACTGTAACTGCTGGAGAT 1750 |
| QY | 1790 | ATAATGGTGAGAAATTCCTATTCGGCTATCAGGAACTTGGGGCCCAATTTGTTTGGGG 1849 |
| Db | 1751 | TTCTTACCGGTAAAGTCCCAATTATGTTTTCAGGCAATTGG---AAATTAGCTTGGACA 1807 |
| QY | 1850 | ACAGGGCTTCTACGACTGCAACCTTCAACTGGACTAAACCTGCTATATTCTTAATCCC 1909 |
| Db | 1808 | GGAATGGAACCAAGTTGGAGAAATTTCTCTGGATAAATAAATTTAAGCCTAGACCT 1867 |
| QY | 1910 | GAGCGTATCGGCTCTTTAGTCCCTAATAGCTTTATGGAATGCAATTTATAGATATTAGCTCT 1969 |
| Db | 1868 | GAAAAAGAGGAAATTTAGTTCTTAATATCTTTGGGGGAATGCTGTAGATGTGAGATCC 1927 |
| QY | 1970 | CTCAATTTCTTATGGAGACTGCAACGAGGGTTTGCAGGAGACCGTGTCTTTTGGTGT 2029 |
| Db | 1928 | TTAATGAGGTTTCAAGAGACCCATGCAATCGAGCTTACAGACAGATCGAGGCTGTGGATC 1987 |
| QY | 2030 | GCTCGATTATCTAACTTCTTCCATAAGGATAGTACAAAACACGACGGGGTTTTCGCCAT 2089 |
| Db | 1988 | GATGGAATTTGGGAATTTCTTCCATGATCTGCTCCCTCCGAGACAATATAGTACCGTCAT 2047 |
| QY | 2090 | TTGAGTGGCGTTATGTATAGGAGGAAACCTACATCTTTGTTTCAGATAAGATTTCTAGT 2149 |
| Db | 2048 | AACAGCGTGGATATGTTCTATCTGTAATAATAGATCAACCTAAGCATACTACTTCG 2107 |
| QY | 2150 | GCTGCATTTTGTAGCTCTTTTGAAGAGATAGAGACTACTTTTGTAGCTTAAGAACTCAAGT 2209 |
| Db | 2108 | ATGCAATTTTCCCAACTCTTTTAGTAGAGACAAAGGACTATGGGTTTCCAAACAGCAATAC 2167 |
| QY | 2210 | ACAGCTACGGAGGAATCTCTATTATCCAGCACACGAAACC----- 2251 |
| Db | 2168 | AGAAATGTTATTTAGGATCGTATCTCTCTCAATATCAACCTCCCTAGGGAATATTTTCGCT 2227 |

Db 369 GTTTGCAAAATACAAAGTTGCTATGCGCACCAAGATGACCTTTAAAGAACCAACACAGA 428
Qy 2548 AGCTCGTGAATTGGAAGTAGCGCTCTGTGAATCTTGCCCTTACTATCGGGATCCGAT 2606
Db 429 AGCGCGGTCTTTGAAAGACGCGATCTTCTCAAGCTTCTGTACTATAGGTATAAAT 487

RESULT 14
US-09-841-132-182
; Sequence 182, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-182

Query Match 4.4%; Score 132.2; DB 9; Length 3021;
Best Local Similarity 48.8%; Pred. No. 1.2e-25;
Matches 544; Conservative 0; Mismatches 523; Indels 48; Gaps 5;

Qy 1776 TGACTCCAGATCTCTATAATGGGTGAGAAATTCATTCACGGCTATCAGGGAACCTTGGGGCC 1835
Db 1952 TGACTCTAGGAATGAGATGCCCTAAGTATGGCTATCAAGGAAGCTGGAAGCTTGGTGGG 2011

Qy 1836 CAATTGTTTGGGGACAGGGGCTTCTACGACTGCAACCTTCACTGGACTAAACCTGGCT 1895
Db 2012 ATCCTAATACAGCAATAATGGTCCCTTATCTGAAAGCTACATGAGACTAAACCTGGGT 2071

Qy 1896 ATATTCTTAATCCGAGCGTATCGGCTCTTGTAGTCCCTAATAGCTTATGGAATGCAATTA 1955
Db 2072 ATAATCCTGGGCGCTGACGAGTAGTCTTCTTGTGTCCTCAATAGTTTATGGGATCCATTT 2131

Qy 1956 TAGATATTAGCTCTCTCCATTATCTTATGAGACTGCAACGAGGCTTGCAGGGAGACC 2015
Db 2132 TAGATATACATCTGCCATTCAGCAATTCAGCAAGTGTGGATGGCGCTCTTATTGTC 2191

Qy 2016 GTGCTTTTGGGTGCTGAGATATCTAACTTCTTCCATAGGATAGTACAAAACAGGAC 2075
Db 2192 GAGGATATGGGTTCTGAGGTTTCGAAATTTCTTCTATCATGACCGCGATGCTTTAGGTC 2251

Qy 2076 GCGGTTTCCCATTTGAGTGGGCTTATGCTAGAGGAAACCTACATCTGTTTCAG 2135
Db 2252 AGGATATCGGTATATTAGTGGGGGTTATTCCTTAGGAGCAAACTCCTCTTTGGATCA - 2310

Qy 2136 ATAGATTTCTTAGTGTGCAATTTGTCAAGCTCTTTGGAAGATAGAGACTCTTTGTAG 2195
Db 2311 --TCGATGTTGGTCTAGCATTTACCGAATTTTGGTAGTCTAAGATTTAGTAGTGT 2368

Qy 2196 CTAGAAATCAAGGTACAGTCTTACGAGGAACCTCTCTATTACCAGCACACAGAAACCTATA 2255
Db 2369 GTCGTTCCAAATCATCATGCTTGCATAGATC-----CGTTTA 2405

Qy 2256 TCTCTCTCTCTGCAAACTAGCGCTTGTGTTGTTCTTATGTTCTCTACAGATTCCTG 2315
Db 2406 TCTATCTACCAACAAGCT-----TTATGTTGATCCCTATTGTTGCGAGATGCGTT 2456

Qy 2316 TTCTCTTTTTCAGGAACCTTATAGCTACACCCATACGGATACGATCTGAAAACCAAGTATA 2375
Db 2457 TATCGGT-----GCTAGCTACGGGTTTGGGAATCAGCATATGAAACCTCATATA 2506

Qy 2376 CAACATATCTACTGTTAAAGBAGCTGGGGAAATGATAGTTTCGCTTTAGAAATTCGGTG 2435
Db 2507 CATTTGAGAGAGAGAGCGATGTTGCTTTGGGATTAATACTGCTGCGCTGGAGAGATTGGAG 2566
Qy 2436 GAAGAGCTCCGATTTGCTTAGATGAAAGTGTCTTANTTTGAGCAGATACATG---CCCTTCA 2492
Db 2567 CGGATTTACGATTTGTGATTACTCCTAAGCTCTATTTGAATGAGTTGGTCTCTTCG 2626

Qy 2493 TGAATTTGCGAGTTTGTCTATGCAATCAGGAAGTTTTAAAGACACAGGACAGAACTC 2552
Db 2627 TGCAAGCTGAGTTTTCTTATGCGGATCATGAATCTTTTACAGAGAAAGGCGATCAAGCTC 2686

Qy 2553 GTGAATTTGGAAGTAGCGGCTCTGTGAATCTTGCTTACCTATCGGATCCGATTTGATA 2612
Db 2687 GGGCATTTCAAGAGCGGACAICTCTCTAATCTATCAGTCTCTGTTGGAGTGAAGTTTGATC 2746

Qy 2613 AGGAATCAGACTGCCAAGATGCAACGCTACAACTTAATCTTCTTGGTTATCTGTGTGATCTTG 2672
Db 2747 GATGTTCTAGTACACATCTCTAATAATATAGCTTTATGGCGCTTATATCTGTGATGCTT 2806

Qy 2673 TTGCTAGTAACCCGAGCTAGTACGACAACTGCGAATTAGCGGTGATTTCTTGGAAACCT 2732
Db 2807 ATCGCACCATCTCTGCTACTGAGACAACGCTCTTATCCATCAAGAGACATGGACAAACG 2866

Qy 2733 TCGGTACGAATTTGGCAGACAAAGCTTTAGTCTCTTGTGCGAGGAACCATTTTGTCTTTA 2792
Db 2867 ATGCTTTTCAATTTAGCAAGACATGGAGTTGTTGGTTAGAGGATCTATGTATGCTTCTCTAA 2926

Qy 2793 ACTCAAAATTTGAAGCCTTTTAGCCAAATTTCTTTTGAATTCGTTGGGTGCTATCTCGCAAT 2852
Db 2927 CAAGTAATATAGAAGTATATGCCATGGAAGATATGATATCGAGATGCTTCTCGAGCT 2986

Qy 2853 ACAATGTAGACTTAGGACCAAAATACCAATCTAA 2887
Db 2987 ATGTTTTCAGTSCAGGAAGTAAAGTCCGGTTCTAA 3021

RESULT 15

US-09-841-132-170
; Sequence 170, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-170

Query Match 4.4%; Score 131.4; DB 9; Length 2949;
Best Local Similarity 48.6%; Pred. No. 1.9e-25;
Matches 542; Conservative 2; Mismatches 523; Indels 48; Gaps 5;

Qy 1776 TGACTCCAGATCTCTATAATGGGTGAGAAATTCATTCACGGCTATCAGGGAACCTTGGGGCC 1835
Db 1880 TGACTCTAGGAATGAGATGCCCTAAGTATGGCTATCAAGGAAGCTGGAAGCTTGGTGGG 1939

Qy 1836 CAATTGTTTGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTGAAAACTGGCT 1895
Db 1940 ATCTTAATACAGCAATAATGTTCTTACTTCTGAAGCTACATGACTAAACTGGGT 1999

Qy 1896 ATATTCTTAATCCGAGCGTATCGGCTCTTGTAGTCCCTAATAGCTTATGGAATGCAATTA 1955
Db 2000 ATAATCCTGGGCTGAGCGAGTAGTCTTCTTGTGTTCCMAATAGTTTATGGGATCCATTT 2059

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OM nucleic - nucleic search, using sw model

Run on: December 16, 2003, 12:16:53 ; Search time 5962 Seconds
(without alignments)

12229.693 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 3000
Sequence: 1 cgccttaccctagtaggt.....tgctttgctaaacactttc 3000

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estnu:*

4: em_estov:*

5: em_estpl:*

6: em_estro:*

7: em_esthc:*

8: em_estl:*

9: gb_estl:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estom:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gsa1:*

29: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| C 1 | 50.6 | 1.7 | 923 | 29 | CNS01509 |
| C 2 | 49.4 | 1.6 | 334 | 9 | AU076383 |
| C 3 | 46.8 | 1.6 | 585 | 9 | AU263143 |
| C 4 | 46.8 | 1.6 | 1201 | 13 | BX336919 |

| | | | | | |
|------|------|-----|------|----|-----------|
| C 5 | 46.2 | 1.5 | 853 | 10 | BF265090 |
| C 6 | 45.4 | 1.5 | 843 | 29 | BZ643413 |
| C 7 | 45.4 | 1.5 | 1201 | 13 | BX376097 |
| C 8 | 44.8 | 1.5 | 391 | 9 | AU263574 |
| C 9 | 44.8 | 1.5 | 720 | 29 | AG088699 |
| C 10 | 44.6 | 1.5 | 592 | 28 | AZ972038 |
| C 11 | 44.4 | 1.5 | 1025 | 29 | CNS014J2 |
| C 12 | 44 | 1.5 | 450 | 12 | BM881804 |
| C 13 | 44 | 1.5 | 498 | 10 | BG602722 |
| C 14 | 44 | 1.5 | 593 | 10 | BG602721 |
| C 15 | 44 | 1.5 | 735 | 12 | BM160527 |
| C 16 | 44 | 1.5 | 767 | 12 | BM657645 |
| C 17 | 43.8 | 1.5 | 596 | 29 | FR0019514 |
| C 18 | 43.8 | 1.5 | 820 | 28 | BH051138 |
| C 19 | 43.6 | 1.5 | 574 | 28 | AZ526815 |
| C 20 | 43.2 | 1.4 | 716 | 12 | BM627037 |
| C 21 | 43.2 | 1.4 | 1101 | 29 | CNS008VI |
| C 22 | 43.2 | 1.4 | 1201 | 13 | BX394744 |
| C 23 | 42.8 | 1.4 | 783 | 29 | CNS00AIS |
| C 24 | 42.8 | 1.4 | 1201 | 29 | CNS0167M |
| C 25 | 42.6 | 1.4 | 1177 | 13 | BX338151 |
| C 26 | 42.4 | 1.4 | 240 | 9 | AU072820 |
| C 27 | 42.4 | 1.4 | 1101 | 29 | CNS0039G |
| C 28 | 42.2 | 1.4 | 660 | 28 | AZ567761 |
| C 29 | 42 | 1.4 | 900 | 28 | AQ744776 |
| C 30 | 42 | 1.4 | 1201 | 13 | BX337161 |
| C 31 | 41.8 | 1.4 | 516 | 10 | BF954368 |
| C 32 | 41.8 | 1.4 | 712 | 13 | BX416727 |
| C 33 | 41.8 | 1.4 | 998 | 13 | BX436885 |
| C 34 | 41.6 | 1.4 | 509 | 12 | BM316139 |
| C 35 | 41.6 | 1.4 | 553 | 9 | AW019090 |
| C 36 | 41.6 | 1.4 | 1101 | 29 | CNS00KF8 |
| C 37 | 41.4 | 1.4 | 480 | 29 | BZ643398 |
| C 38 | 41.4 | 1.4 | 926 | 28 | BH156551 |
| C 39 | 41.4 | 1.4 | 948 | 13 | BX414840 |
| C 40 | 41.4 | 1.4 | 1101 | 29 | CNS017NE |
| C 41 | 41.4 | 1.4 | 1201 | 13 | BX384793 |
| C 42 | 41.2 | 1.4 | 703 | 12 | BM602748 |
| C 43 | 41.2 | 1.4 | 1201 | 13 | BX462660 |
| C 44 | 41 | 1.4 | 529 | 10 | BE225902 |
| C 45 | 41 | 1.4 | 735 | 29 | CNS04NSM |

ALIGNMENTS

RESULT 1
CNS01509/c

LOCUS

DEFINITION

CNS01509 923 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN14B20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

VERSION AL105699.1 GI:5617836

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 923)

AUTHORS

TITLE

JOURNAL

COMMENT

Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector

BR265090 HV_CEA001
BZ643413 OGJOM57TM
BX376097 BX376097
AU263574 AU263574
AG088699 Pan trogl
AZ972038 2M0245R13
AL104216 Drosophil
BM881804 rbi4b09.y
BG602722 EST501812
BG602721 EST501811
BM160527 EST563050
BM657645 170006874
AL012404 F.rubripe
BH051138 RPCI-24-3
AZ526815 2605bA10
AL052689 Drosophil
BX394744 BX394744
AL055833 Drosophil
AL106396 Drosophil
BX338151 BX338151
AU072820 AU072820
AL063921 Drosophil
AZ567761 238PVG08
AQ744776 HS 5506.A
BF954368 QV2-NN004
BX416727 BX416727
BX436885 BX436885
BM316139 fw70a01.x
AW019090 fd59G04.x
AL077903 Drosophil
BZ643398 OGAOW57TC
BH156551 ENTID75TR
BX414840 BX414840
AL108260 Drosophil
BX384793 BX384793
BM602748 170006870
BX462660 BX462660
BE225902 la21C12.x
AL299119 Tetraodon

FEATURES
source

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Qy 38 TTGTTCTCCTATGCGTATCTCTTAAATATATAATCAAAATCAAGTATATTTT 97
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584 TTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 525
Qy 98 ARAATGAAGCTCTCTTCCCAAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 157
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
524 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 465
Qy 158 ATGATTCGCTACCGAGACAGTTTTCGATTCAGTTCGAGTTTCGATTCGAGTTCG 217
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464 AGATATTCGCTACACCTTTATTAGATTCGAATGTTCTTTCAGAGAATCAATGTTGG 405
Qy 218 AATTTTCAGTTCGTGAGAGTCAGAGAGAGCTCGAACTACCTACCTATTTAAAGGGAAT 277
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404 AACTTACCATTTGTTAAGAGATCAGCAATGTTAAACATACCAATGTTATTCATAA 345
Qy 278 GTCACTCTAGAAATATTCCTGGAACAGGCACACCAATCA 319
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
344 GCAACATAACATATAAATCAGCCAAAGTGAAGAATTACCA 303

RESULT 4
LOCUS BX336919
DEFINITION BX336919 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI033YL20 5-PRIME, mRNA sequence.
ACCESSION BX336919.1 GI:30345558
VERSION BX336919
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
TITLE Li W.B., Gruber C., Jessee J. and Polayes D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2019.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI033DF10QP1&cluster=2019.r. Contact :
Feng liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI033DF10QPI.
Location/Qualifiers
1..1201
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI033YL20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 317 a 228 c 196 g 375 t 85 others
ORIGIN

Query Match 1.6%; Score 46.8; DB 13; Length 1201;
Best Local Similarity 39.4%; Pred. No. 12;
Matches 85; Conservative 36; Mismatches 95; Indels 0; Gaps 0;

Qy 14 TAGAGTTGAGTGAATTTCTGACTGTTTCTCCTATTGTTGTTGTTGTTGTTGTTGTT 73
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846 WATWBSTTTTAAWTTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWTWT 905

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Qy 74 ATTCAAAATCAAAGTATATATTTTCAATGAAGTCTTTCCCAAGTTGTTATTTCT 133
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906 ATAAATWAAATWTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 965
Qy 134 ACATTTGCTATTTTCCCTTTGCTCTATGATTCGACGAGACAGTTTGGATTCAGTGG 193
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
966 TTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1025
Qy 194 AGTTTCGATCGGAATAAATAATGTAATTTTCAGTT 229
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1026 ATAAATAATTTTTHWHTTTTTHWHTTTTTHWHTTTTTHWHTTTTTHWHTTTTTHW 1061

RESULT 5
LOCUS BF265090/c
DEFINITION BF265090 853 bp mRNA linear EST 23-OCT-2001
HV CEA0011D22f Hordeum vulgare seedling green leaf EST library
cDNA clone HV_CEA0011D22f, mRNA sequence.
ACCESSION BF265090
VERSION BF265090.3 GI:16334636
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 853)
REFERENCE Wing R., Close T.J., Kleinhofs A., Wise R., Wei F., Begum D.,
AUTHORS Frisch D., Yu Y., Henry D., Palmer M., Rambo T., Simmons J., Choi
D.W., Fenton R.D., Oates R. and Main D.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla13)
seedling leaf cDNA library
JOURNAL Unpublished
COMMENT On Nov 17, 2000 this sequence version replaced gi:13261889.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 280
Seq primer: AATTACCTCCTACTTAAGG
High quality sequence stop: 831.
Location/Qualifiers
1..853
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Cili16155 (Mla13)"
/db_xref="taxon:112509"
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library HVCDNA0004 (Blumeria challenged)"
/notes="vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
C.I. 16155 (Mla13) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate A27 (AvrMla13
of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;
uninoculated leaves were harvested 20 hr post-inoculation
(Wei, Wise). In the TJ Close lab at the University of
California, Riverside, total RNA was prepared from each
sample pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
cDNA library was made, and 1 million pfu were in vivo
excised to give pBluescript SK(-) cDNA phagemids (Choi,
Close). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA

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FEATURES
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        Location/Qualifiers
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BASE COUNT
ORIGIN

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Best Local Similarity 8.8%; Pred. NO. 26;
Matches 52; Conservative 236; Mismatches 299; Indels 1; Gaps 1;

[illegible]

[illegible]

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 593)
Kappe, S.H.I., Gardner, M.J., Brown, S.M., Ross, J., Matuschewski, K.,
Ribeiro, J.M., Adams, J.H., Quackenbush, J., Cho, J., Carucci, D.J.,
Hoffman, S.L. and Nussenzweig, V.
Exploring the transcriptome of the malaria sporozoite stage
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9895-9900 (2001)

21396555
MEDLINE
PUBMED
11493695
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208

Email: gardner@tigr.org
Request for clones, please contact: Stefan Kappe, Division,
kappe01@popmail.med.nyu.edu Michael Heidelberger, Division,
Department of Pathology New York University School of Medicine.

Location/Qualifiers

1. 593
/organism="Plasmodium yoelii"
/mol_type="mRNA"
/strain="17XL"
/db_xref="taxon:5861"
/clone="PYCDJ76"
/dev_stage="sporozoites from salivary gland"
/lab_host="E. coli TOP10"
/clone_lib="Plasmodium yoelii sporozoite cDNA"
/notes="Vector: pCR4; TA cloning; Plasmodium yoelii
sporozoite cDNA library from salivary gland sporozoites 14
days post-infection"

BASE COUNT 261 a 72 c 70 g 190 t

ORIGIN

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Best Local Similarity 56.1%; Pred. No. 47;
Matches 83; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 15 AGAGGTTGAGTGAATTCCTGACCTGTTCTCCPATTGGTGTATCTCTTAAATATATAA 74
DB 209 AGTGGCTATTTATCTTGTATTTTCTAGCTCTTACATTTCTCAATATTTT 150
QY 75 TTCAAAATCAAGTATATATTTTCAATGAAGTCTTCTTCCCAAGTTGTATTTCTA 134
DB 149 TATCAAAATATACTACTTTTCTTTTATTAAGTATTTTGTCTAATTCGTTTTCGT 90
QY 135 CATTGCTATTTCCCTTGTCTATGAT 162
DB 89 TTATCGTTTCTTATCTTTCTTTTCAT 62

RESULT 15
BM160527/c
LOCUS
DEFINITION
EST563050 PyBS Plasmodium yoelii yoelii cDNA clone PYCJ547 5' end,
mRNA sequence.
ACCESSION
BM160527
VERSION
BM160527.1 GI:17306208
KEYWORDS
EST.
ORGANISM
Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 735)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
Fraser, C.M. and Carucci, D.J.
Plasmodium yoelii EST project at TIGR
Unpublished
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319

Fax: 301-838-0208

Email: carlton@tigr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADP.

Location/Qualifiers

1. 735
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
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/db_xref="taxon:73239"
/clone="PYCJ547"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/cByJ mice infected with Pyl17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose columns. Total RNA was
isolated using the guanidinium isothiocyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybridZAP arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was
excised from the HybridZAP vector and plasmid DNA
isolated."

BASE COUNT 313 a 80 c 84 g 258 t

ORIGIN

Query Match 1.5%; Score 44; DB 12; Length 735;
Best Local Similarity 56.1%; Pred. No. 49;
Matches 83; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
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DB 202 AGTGGCTATTTATCTTGTATTTTCTAGCTCTTCTTACATTTCTTCAATATTTT 143
QY 75 TTCAAAATCAAGTATATATTTTACATGAAGTCTTCTTCCCAAGTTGTATTTCTA 134
DB 142 TATCAAAATATACTACTTTTCTTTTATTAAGTATTTTGTCTAATTCGTTTTCGT 83
QY 135 CATTGCTATTTCCCTTGTCTATGAT 162
DB 82 TTATCGTTTCTTATCTTTCTTTTCAT 55

Search completed: December 16, 2003, 17:14:31
Job time : 5967 secs

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 16, 2003, 10:21:33 ; Search time 80.5 Seconds
(without alignments)
11830.552 Million cell updates/sec

Title: US-09-428-122-1

Perfect score: 5409

Sequence: 1 cgccttaactagtagaggt.....tggtttgtctaaacactttc 3000

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 2215726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool.p/US09428122/runat_16122003_102127_10757/app.query.fasta_1.3143
-DB-A Geneseq 19Jun03 -CFMT=fastap -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09428122_@CGN 1.104 @runat_16122003_102127_10757 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|--------|-------|--------|----|----------|----------------------|
| 1 | 4774 | 88.3 | 928 | 21 | AAV94327 | Chlamydia pneumoniae |
| 2 | 4760 | 88.0 | 928 | 21 | AAW88421 | Chlamydia pneumoniae |
| 3 | 3865 | 71.5 | 746 | 23 | ABB90535 | Chlamydia pneumoniae |
| 4 | 2997 | 55.4 | 597 | 20 | AAV34611 | Chlamydia pneumoniae |
| 5 | 2058 | 38.0 | 928 | 20 | AAW88418 | Chlamydia pneumoniae |
| 6 | 2048 | 37.9 | 928 | 23 | ABB90573 | Chlamydia pneumoniae |
| 7 | 2021 | 37.4 | 928 | 21 | AAV90237 | Chlamydia pneumoniae |
| 8 | 2006 | 37.1 | 918 | 21 | AAV93669 | Amino acid sequenc |
| 9 | 2001 | 37.0 | 918 | 20 | AAW88422 | Chlamydia pneumoniae |
| 10 | 1993 | 36.8 | 914 | 20 | AAW88429 | Chlamydia pneumoniae |
| 11 | 1987.5 | 36.7 | 885 | 21 | AAV90238 | Mature Chlamydia a |
| 12 | 1986 | 36.7 | 928 | 20 | AAW88423 | Chlamydia pneumoniae |
| 13 | 1982 | 36.6 | 928 | 23 | ABB90542 | Chlamydia pneumoniae |
| 14 | 1976 | 36.5 | 928 | 21 | AAV90239 | Chlamydia pneumoniae |
| 15 | 1965 | 36.3 | 936 | 21 | AAV99842 | Chlamydia pneumoniae |
| 16 | 1965 | 36.3 | 936 | 23 | ABB90602 | Chlamydia pneumoniae |
| 17 | 1946.5 | 36.0 | 925 | 21 | AAV99843 | Chlamydia pneumoniae |
| 18 | 1940 | 35.9 | 930 | 20 | AAV35052 | Chlamydia pneumoniae |
| 19 | 1936 | 35.8 | 930 | 23 | ABB90548 | Chlamydia pneumoniae |
| 20 | 1930 | 35.7 | 930 | 21 | AAV90240 | Chlamydia pneumoniae |
| 21 | 1927 | 35.6 | 930 | 20 | AAW88424 | Chlamydia pneumoniae |
| 22 | 1917.5 | 35.5 | 927 | 20 | AAV35054 | Chlamydia pneumoniae |
| 23 | 1915 | 35.4 | 926 | 23 | ABP56019 | Chlamydia peittaci |
| 24 | 1915 | 35.4 | 926 | 23 | ABB98228 | Chlamydia polypt |
| 25 | 1915 | 35.4 | 926 | 24 | ABU66284 | C. peittaci protei |
| 26 | 1871 | 34.6 | 949 | 20 | AAV35060 | Chlamydia pneumoniae |
| 27 | 1855 | 34.3 | 928 | 20 | AAW88417 | Chlamydia pneumoniae |
| 28 | 1855 | 34.3 | 928 | 21 | AAV90236 | Chlamydia pneumoniae |
| 29 | 1855 | 34.3 | 928 | 23 | ABB90583 | Chlamydia pneumoniae |
| 30 | 1832 | 33.9 | 945 | 21 | AAV69368 | Amino acid sequenc |
| 31 | 1811 | 33.5 | 945 | 20 | AAW88428 | Chlamydia pneumoniae |
| 32 | 1659.5 | 30.7 | 839 | 23 | ABP56002 | Chlamydia peittaci |
| 33 | 1659.5 | 30.7 | 839 | 23 | ABB98211 | Chlamydia polypt |
| 34 | 1659.5 | 30.7 | 839 | 24 | ABU66267 | C. psittaci protei |
| 35 | 1580.5 | 29.2 | 841 | 23 | ABB90595 | Chlamydia pneumoniae |
| 36 | 1577.5 | 29.2 | 841 | 21 | AAV92818 | C. pneumoniae CPN1 |
| 37 | 1575.5 | 29.1 | 841 | 20 | AAW88420 | Chlamydia pneumoniae |
| 38 | 1572.5 | 29.1 | 643 | 20 | AAV35056 | Chlamydia pneumoniae |
| 39 | 1442.5 | 26.7 | 922 | 23 | ABB90546 | Chlamydia pneumoniae |
| 40 | 1437.5 | 26.6 | 922 | 21 | AAV95548 | Chlamydia pneumoniae |
| 41 | 1430.5 | 26.4 | 922 | 20 | AAW88419 | Chlamydia pneumoniae |
| 42 | 1417.5 | 26.2 | 922 | 20 | AAV34597 | Chlamydia pneumoniae |
| 43 | 1383.5 | 25.6 | 1407 | 23 | ABB90541 | Chlamydia pneumoniae |
| 44 | 1377.5 | 25.5 | 973 | 21 | AAV96274 | Chlamydia POMP91B |
| 45 | 1377.5 | 25.5 | 973 | 23 | ABB90527 | Chlamydia pneumoniae |

ALIGNMENTS

RESULT 1
AAV94327
ID AAV94327 standard; Protein; 928 AA.
AC AAV94327;
XX
XX
XX
XX 11-AUG-2000 (first entry)
XX
XX Chlamydia pneumoniae 98kD putative outer membrane protein.
XX
XX Chlamydia; antigen; vaccine; infection; outer membrane protein.
XX Chlamydia pneumoniae.
XX Chlamydia pneumoniae.
XX WO200026237-A2.
XX
XX 11-MAY-2000.
XX

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PF 29-OCT-1999; 99WO-GB03579.
XX
PR 29-OCT-1998; 98US-0106070.
PR 01-MAR-1999; 99US-0122066.
PR 27-OCT-1999; 99US-0428122.
XX
XX (CONN-) CONNAUGHT LAB LTD.
PA
PI
PI Murdin AD, Oomen RP, Dunn PL;
XX
XX WPI: 2000-365569/31.
DR N-PSDB; AAR27021.
XX
XX Novel Chlamydia 98 kDa putative outer membrane protein antigen, used
PT for vaccination and protection against Chlamydia infection -
PT
PS Claim 6; Fig 1; 93pp; English.
XX
XX The present sequence is the 98kDa putative outer membrane protein from
CC Chlamydia pneumoniae. The genomic sequence was amplified using two
CC PCR primers. The 5' primer contains a NotI restriction site, a ribosome
CC binding site, an initiation codon and a sequence close to the 5' end of
CC the 98kDa putative outer membrane protein coding sequence. The 3' primer
CC contains the sequence encoding the C-terminal sequence of the putative
CC outer membrane protein and a BstXI restriction site. The stop codon was
CC excluded and an additional nucleotide was inserted to obtain an in-frame
CC C-terminal fusion with the Histidine tag. The PCR product was cloned
CC into a eukaryotic expression vector (pCA-Myc-His) by restricting both
CC the vector and the PCR product with NotI and BamHI and performing a
CC ligation reaction. This expression vector was injected intramuscularly
CC and intranasally into mice, which were subsequently inoculated with
CC Chlamydia pneumoniae. The chlamydial lung titers of the immunised mice
CC were lower than those of the controls. Thus the 98kDa putative outer
CC membrane protein can be used as a vaccine to provide protection against
CC Chlamydia infections, especially Chlamydia pneumoniae infections.
CC The present polypeptide may also be administered orally to treat
XX Chlamydia infection.
XX
SQ Sequence 928 AA;

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Alignment Scores:

| Pred. No.: | Score: | Length: |
|------------------------|---------|-----------------|
| 0 | 4774.00 | 928 |
| Percent Similarity: | 100.00% | Matches: 928 |
| Best Local Similarity: | 100.00% | Conservative: 0 |
| Query Match: | 88.26% | Mismatches: 0 |
| DB: | 21 | Indels: 0 |
| | | Gaps: 0 |

US-09-428-122-1 (1-3000) x AAY94327 (1-928)

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QY 161 ATTGCTACCGACAGATTTGGATTTCAGTCCGAGTTTCGATGGGAATAAATGGTAAT 220
Db 21 IleAlaThrGluThrValLeuAspSerSerAlaSerPheAspGlyAsnLysAsnGlyAsn 40
QY 221 TTTTCAGTTCTGTAGAGTCAGCAAGATGCTGGAACTACCTACTATTATTAAGGAAATGTC 280
Db 41 PheSerValArgGluSerGlnGluAspAlaGlyThrThrThrLeuPheLysGlyAsnVal 60
QY 281 ACTCTAGAAAATATTCTCTGGAACAGGCACAGCAATACAAAAGCTGTTTAAACAACT 340
Db 61 ThrLeuGluAsnIleProGlyThrGlyThrAlaIleThrLysSerCysPheAsnAsnThr 80
QY 341 AAGCGGATTTGACTTTTCACAGGTAAACGGAACTCTCTATTGTTCCAAACCGTGGATGCA 400
Db 81 LysGlyAspLeuThrPheThrGlyAsnGlyAsnSerLeuLeuPheGlnThrValAspAla 100
QY 401 GGGACTGTAGCAGGGGCTGTGTTTAACAGCAGCGTGGTAGATAATCTTACCACCGTTTATA 460
Db 101 GlyThrValAlaGlyAlaValAsnSerSerValValAspLysSerThrThrPheIle 120

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461 GGGTTTCTTCGCTATCTTTTATTGCGTCTCCTCGAAGTTTCGATAACTACGGCAAGGA 520

121 GlyPheSerSerLeuSerPheIleAlaSerProGlySerSerIleThrThrGlyLysGly 140

521 GCCGTTAGCTGCTCTACGGGTAGCTTTCAGTTTGCACAAAAATGTCAGTTCTCTTCAGC 580

141 AlaValSerCysSerThrGlySerLeuSerLeuThrLysAsnValSerLeuPheSer 160

581 AAAAATCTTTTCAACGGATAATGGCGGTGCTATACCCGCAAAAACTCTTTCATTACACGG 640

161 LysAsnPheSerThrAspAsnGlyGlyAlaIleThrAlaLysThrLeuSerLeuThrGly 180

641 ACTCAATGTCAGCTCTGCTTTCTGAAATACCTCTCAAGAGAGGGGGAGCCATTTCAG 700

181 ThrThrMetSerAlaLeuPheSerGluAsnThrSerSerLysLysGlyGlyAlaIleGln 200

701 ACTCCGATGCCCTTACCATTACTGGAACCAAGGGGAGTCTCTTTTCTGCACAACTACT 760

201 ThrSerAspAlaLeuThrIleThrGlyAsnGlnGlyGluValSerPheSerAspAsnThr 220

761 TCTTCGGATTCTCGAGCTGCAATTTTACAGAGCTCGGTGACTATTTCTTAATTAATGCT 820

221 SerSerAspSerGlyAlaAlaIlePheThrGluAlaSerValThrIleSerAsnAla 240

821 AAGATTCTCTTATTGACAATAAGGTCAAGAGCGAGCTCTCAACACGGGGGATATG 880

241 LysValSerPheIleAspAsnLysValThrGlyAlaSerSerSerThrThrGlyAspMet 260

881 TCAGGAGTGTCTATCTGCTTATAAACTAGTACAGATACTAGGTCAACCTCACTGGA 940

261 SerGlyGlyAlaIleCysAlaLysThrSerThrAspThrLysValThrLeuThrGly 280

941 AATCAGATGTTACTCTTCAGCAACATACATCGACACAGCGGGAGGACTATCTATG 1000

281 AsnGlnMetLeuLeuPheSerAsnAsnThrSerThrThrAlaGlyGlyAlaIleThrVal 300

1001 AAAAGCTCGAATGCTGCTTCCGAGGACTTACCTTATTCAGTAGAAATAGTGTCAATGA 1060

301 LysLysLeuGluLeuAlaSerGlyGlyLeuThrLeuPheSerArgAsnSerValAsnGly 320

1061 GGTACAGCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAATGAGTTTATCC 1120

321 GlyThrAlaProLysGlyGlyAlaIleAlaIleGluAspSerGlyGluLeuSerLeuSer 340

1121 GCCGATAGTGTGACATTTGCTTTTTCAGGAATACAGTCACTTCTACTACTCTCTGGAG 1180

341 AlaAspSerGlyAspIleValPheLeuGlyAsnThrValThrSerThrThrProGlyThr 360

1181 AATAGAAGTAGTATCGACTTAGCAACGAGTCAGCAAGATGACAGCTTTGGTCTGCTGCT 1240

361 AsnArgSerSerIleAspLeuGlyThrSerAlaLysMetThrAlaLeuArgSerAlaAla 380

1241 GGTAGAGCCATCTACTCTATGATCCCAATACATACAGGATCATCCACACAGTTACAGAT 1300

381 GlyArgAlaIleThrPheThrAspProIleThrThrGlySerSerThrThrValThrAsp 400

1301 GTCTTAAAGTTAATGAGCTCCGAGATTCCTGCACTCAATATACAGGACATCATC 1360

401 ValLeuLysValAsnGluThrProAlaAspSerAlaLeuGlnThrThrGlyAsnIleIle 420

1361 TTCACAGGAGAAAAGTTATCAGAGACAGAGCGCCGAGATCTCTAAAATCTTACTTGAAG 1420

421 PheThrGlyGluLysLeuSerGluThrGluAlaAlaAspSerLysAsnLeuThrSerLys 440

1421 CTACTACAGCTGTAACTCTTTTCAGGAGGTACTCTATCTTTTAAACAATGAGGTACTCTG 1480

441 LeuLeuGlnProValThrLeuSerGlyGlyThrLeuSerLeuLysHisGlyValThrLeu 460

1481 CAGACTCAGGCACTTCACTCAACAGGCGAGTCTCTGCTCCGAATGGACGTAGGAAGTACT 1540

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1541 CTAGAACCTGCTGATACCTAGCACCATAAACAATTTGGTCATTAAACATCAGTTCATAGAC 1600
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 541 GlnSerTyrAspIleLeuGluLeuLysAlaSerGlyThrValThrSerThrAlaValThr 560
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 1961 ATTAGCTCTCTCCATTTCTTATGGAGACTGCAAAACGAAGGTTGCAGGAGACCGTGCT 2020
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841 AspCysGlnAspAlaThrTyrAsnLeuThrLeuGlyTyrThrValAspLeuValArgSer 860
 2681 AACCCCGACTGTACGACAACTCGAATTAGCGGTGATTCTTGAAACACTTCGGTAGC 2740
 861 AsnProAspCysThrThrThrLeuArgIleSerGlyAspSerTrpLysThrPheGlyThr 880
 2741 AATTTGGCAAGACAGCTTTAGTCTCTGTCGAGGGAACCATTTTGTCTTAACTCAAAAT 2800
 881 AsnLeuAlaArgGlnAlaLeuValLeuArgAlaGlyAsnHisPheCysPheAsnSerAsn 900
 2801 TTTGAAGCCTTTAGCCAATTTTTCATTTGCAATTTGCGTGGGTGATCTCGCAATTTACAATGTA 2860
 901 PheGluAlaPheSerGlnPheSerPheGluLeuArgGlySerSerArgAsnTyrAsnVal 920
 2861 GACTTAGGAGCAAAATACCAATTC 2884
 921 AspLeuGlyAlaLysTyrGlnPhe 928
 RESULT 2
 AAW88421
 ID AAW88421 standard; Protein; 928 AA.
 XX AC AAW88421;
 XX DT 26-APR-1999 (first entry)
 XX DE Chlamydia pneumoniae surface exposed protein Omp8.
 XX KW Omp8; outer membrane protein 8; surface exposed protein; antigen;
 XX KW infection; diagnosis; vaccine; atherosclerosis; asthma.
 XX OS Chlamydia pneumoniae.
 XX PN WO9858953-A2.
 XX DD 30-DEC-1998.
 XX PF 19-JUN-1998; 98WO-DK00266.
 XX PR 23-JUN-1997; 97DK-0000744.
 XX PA (BIRK/) BIRKELUND S.
 XX PA (CHRI/) CHRISTIANSEN G.
 XX PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
 XX PI Mygind P;
 XX DR WPI; 1999-105610/09.
 XX DR N-PSDB; AAX06820.
 XX PT Species-specific test for identifying mammals infected with
 PT Chlamydia pneumoniae - comprises detecting antibodies specific for
 PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
 PT these proteins
 XX Claim 7; Page 53-55; 115pp; English.
 XX This polypeptide comprises the novel 90.0 kDa surface exposed
 XX protein Omp8 of the human respiratory pathogen Chlamydia
 XX pneumoniae. Its amino acid sequence was deduced from DNA (see
 XX AAX06820) isolated from a C. pneumoniae expression library. The
 XX invention provides 12 novel surface exposed proteins, Omp4-Omp15
 XX (see AAW88417-28), and nucleic acid sequences encoding them (see
 XX AAX06816-27). A new species specific test is claimed that is used
 XX to identify mammals (including humans) infected with Chlamydia
 XX pneumoniae. The test comprises detecting antibodies specific for
 XX Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
 XX membrane proteins, especially by PCR. The proteins are also used
 XX in the diagnosis of C. pneumoniae infection in mammals. The
 XX nucleic acids and proteins can also be used in the immunization of
 XX mammals, the nucleic acids being particularly useful as DNA
 XX vaccines for effecting in vivo expression of antigens. The

CC vaccines may also prevent atherosclerosis and bronchial asthma,
 CC which are possibly associated with C. pneumoniae.

XX Sequence 928 AA;

Alignment Scores:
 Pred. No.: 0 Length: 928
 Score: 4760.00 Matches: 925
 Percent Similarity: 99.68% Conservative: 0
 Best Local Similarity: 99.68% Mismatches: 3
 Query Match: 88.00% Indels: 0
 DB: 20 Gaps: 0

US-09-428-122-1 (1-3000) x AAW88421 (1-928)

QY 101 ATGAAGTCTCTTCCCAAGTTTGTATTTCTACATTTGCTATTTCCCTTCTCTATG 160
 Db 1 MetLysSerSerPheProLysPheValPheSerThrPheAlaIlePheProLeuSerMet 20
 QY 161 ATTGCTACCGAGACAGTTTTCGATTCAAGTCCGAGTTTCGATGGGAATATAAATGGTAAT 220
 Db 21 IleAlaThrGluThrValLeuAspSerSerAlaSerPheAspGlyAsnLysAsnGlyAsn 40
 QY 221 TTTTCAGTTCGTGAGTGCAGAGATGCTGAACTACCTACTATTTTAAGGGAAATGTC 280
 Db 41 PheSerValAlaGluSerGlnGluAspAlaGlyThrThrThrLeuPheLysGlyAsnVal 60
 QY 281 ACTCTAGAAAAATATTCCTGGCAACAGCACAGCAATCACAAAAAGCTGTTTTAACAACT 340
 Db 61 ThrLeuGluAsnIleProGlyThrGlyThrAlaIleThrLysSerCysPheAsnAsnThr 80
 QY 341 AAGGCGATTTCAGCTTTCACAGTTAACGGGAAGTCTCTATTTGTTCCAAACGGTGGATCA 400
 Db 81 LysGlyAspLeuThrPheThrGlyAsnGlyAsnSerLeuLeuPheGlnThrValAspAla 100
 QY 401 GGGACTGTAGCAGGGGCTGTTTAAACAGACGCGGTAGATAAATCTACCACTGTTTATA 460
 Db 101 GlyThrValAlaGlyAlaValAsnSerSerValValAspLysSerThrThrPheIle 120
 QY 461 GGGTTTCTTCGCTATCTTTTATTCGCTCTCTCGAAGTTCGATAACTACCGGCAAGGA 520
 Db 121 GlyPheSerSerLeuSerPheIleAlaSerProGlySerSerIleThrThrGlyLysGly 140
 QY 521 GCGGTTAGTCTCTACGGGTAGCTTGAGTTTGAACAAAAGTCTGAGTTGCTCTCTCAGC 580
 Db 141 AlaValSerCysSerThrGlySerLeuLysPheAspLysAsnValSerLeuLeuPheSer 160
 QY 581 AAAAATTTTCAACGGTAATGCGGTGCTATCACCGCAAAATCTTTTCATTAACAGGG 640
 Db 161 LysAsnPheSerThrAspAsnGlyGlyAlaIleThrAlaLysThrLeuSerLeuThrGly 180
 QY 641 ACTACAATGTCAGCTCTGTTTTCTGAAAATACCTCTCAAGAAAGGCGGAGCCATTGAG 700
 Db 181 ThrThrMetSerAlaLeuPheSerGluAsnThrSerSerLysLysGlyAlaIleGln 200
 QY 701 ACTTCGATGCCCTTACCAATTACTGAAACCAAGGGAAGTCTCTTTTCTGACATACT 760
 Db 201 ThrSerAspAlaLeuThrIleThrGlyAsnGlnGlyValSerPheSerAspAsnThr 220
 QY 761 TCTTCGGATTCTGGAGCTGCAATTTTACAGAAGCTCGTGACTATTTCTAATAATGCT 820
 Db 221 SerSerAspSerGlyAlaAlaIlePheThrGluAlaSerValThrIleSerAsnAla 240
 QY 821 AAAATTTCTTTTATGACAATAAGGTACAGGAGCGAGTCTCTCAACACGCGGGATATG 880
 Db 241 LysValSerPheIleAspAsnLysValThrGlyAlaSerSerSerThrThrGlyAspMet 260
 QY 881 TCAGGAGGTGCTATCTGTGCTTTTAAACCTAGTACAGATCTAAGTCTACCTCCTCTGGA 940
 Db 261 SerGlyGlyAlaIleCysAlaThrLysThrSerThrAspThrLysValThrLeuThrGly 280
 QY 941 AATCAGATGTACTCTTCAGCAACATATACACACACGCGGAGGAGCTATCTATG 1000

Db 281 AsnGlnMetLeuLeuPheSerAsnAsnThrSerThrThrAlaGlyGlyAlaIleTyrVal 300
 QY 1001 AAAAAGCTCGAAGTCTTCCGGAGAGACTTACCTATTTCAGTAGAAATAGTGTCAATGGA 1060
 Db 301 LysLysLeuGluLeuAlaSerGlyGlyLeuThrLeuPheSerArgAsnSerValAsnGly 320
 QY 1061 GGTACAGCTCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAATTTGAGTTTATCC 1120
 Db 321 GlyThrAlaProLysGlyGlyAlaIleAlaIleGluAspSerGlyGluLeuSerLeuSer 340
 QY 1121 GCCGATAGTGGTCACATTTGTTTTAGGGAATACAGTCACTTCTACTCTCTCTGGAGC 1180
 Db 341 AlaAspSerGlyAspIleValPheLeuGlyAsnThrValThrSerThrThrProGlyThr 360
 QY 1181 AATAGAAGTAGTATCGACTTAGGAACGAGTGCAGAAAGATGACAGCTTGGCTTCTGGTCT 1240
 Db 361 AsnArgSerSerIleAspLeuGlyThrSerAlaLysMetThrAlaLeuArgSerAlaAla 380
 QY 1241 GGTAGAGCCATCTCTTCTATGATCCCATAACTACAGGATCATCCACACAGTTACAGAT 1300
 Db 381 GlyArgAlaIleTyrPheTyrAspProIleThrThrGlySerSerThrThrValThrAsp 400
 QY 1301 GTCTTAAAGTTAATGAGACTCCGGCAGATTCGCTACTACAATATACAGGGAACATCATC 1360
 Db 401 ValLeuLysValAsnGluThrProAlaAspSerAlaLeuGlnTyrThrGlyAsnIleIle 420
 QY 1361 TTCACAGGAAAGTTATCAGAGACAGAGCCGACAGTCTTAAATCTTACTTCGGAAG 1420
 Db 421 PheThrGlyGluLysLeuSerGluThrGluAlaAlaAspSerLysAsnLeuThrSerLys 440
 QY 1421 CTACTACAGCTGTAACTCTTTTCAGGAGGTACTCTATCTTTAAACATGAGTGACTCTG 1480
 Db 441 LeuLeuGlnProValThrLeuSerGlyGlyThrLeuSerLeuLysHisGlyValThrLeu 460
 QY 1481 CAGACTCAGGATTCATCAACAGGAGATTCCTCGTCTCGAAATGAGGACTAGGAACTACT 1540
 Db 461 GlnThrGlnAlaPheThrGlnGlnAlaAspSerArgLeuGluMetAspValGlyThrThr 480
 QY 1541 CTGAAGCTGCTGATCTAGCACCATAAACAATTTGGTCATTAACTACATCAGTTCTATAGAC 1600
 Db 481 LeuGluProAlaAspThrSerThrIleAsnAsnLeuValIleAsnIleSerSerIleAsp 500
 QY 1601 GGTCAAGAGAGGCAAAATAGAAACCAAGCTACGTCAAAAATCTGACTTTATCTGGA 1660
 Db 501 GlyAlaLysLysAlaLysIleGluThrLysAlaThrSerLysAsnLeuThrLeuSerGly 520
 QY 1661 ACCATCTATTTATGGACCCCGACCGGACGTTTATGAAATCATAGTTTAAAGAAATCCT 1720
 Db 521 ThrIleThrLeuLeuAspProThrGlyThrPheTyrGluAsnHisSerLeuArgAsnPro 540
 QY 1721 CAGCTCTACGACATCTTAGAGCTCAAGCTTCTGAACTGTAACAGCACCGCAGTGAAT 1780
 Db 541 GlnSerTyrAspIleLeuGluLeuLysAlaSerGlyThrValThrSerThrAlaValThr 560
 QY 1781 CCAGATCTCTATAATGGGTGAGAAATTCATTCAGGCTATCAGGGAACCTTGGGGCCCAAT 1840
 Db 561 ProAspProIleMetGlyLysPheHisTyrGlyTyrGlnGlyThrTyrGlyProIle 580
 QY 1841 GTTGGGGGACAGGGGCTTACGACTCAACCTTCACTGGAATAAACTGGCTATATT 1900
 Db 581 ValTyrGlyThrGlyAlaSerThrThrAlaThrPheAsnThrThrLysThrGlyThrIle 600
 QY 1901 CCTAATCCGAGCGTATCGGCTCTTTTACTCTTATAGCTTATGAAATGCAATTTATAGAT 1960
 Db 601 ProAsnProGluArgIleGlySerLeuValProAsnSerLeuThrPheAlaIleAsp 620
 QY 1961 ATTAGCTCTCTCCATTTATCTTATGAGAGCTGCAAAACGAAAGGTTTCAGGAGACCGTCT 2020
 Db 621 IleSerSerLeuHisTyrLeuMetGluThrAlaAsnGluGlyLeuGlnGlyAspArgAla 640
 QY 2021 TTTTGGTGTGCTGATTTACTTAATCTTCCATAAGGATAGTACAAAACACAGCAGCGGG 2080
 Db 641 PheTyrCysAlaGlyLeuSerAsnPhePheHisLysAspSerThrLysThrArgArgGly 660

QY 2081 TTTCCGCAATTTAGTGGCGTTATGTCATAGGAGGAACTACATACCTACTACTGTTCCAGATAAG 2140
 Db 661 PheArgHisLeuSerGlyGlyTyrValIleGlyGlyAsnLeuHisThrCysSerAspLys 680
 QY 2141 ATTCTTAGTCTGCATTTCTAGCTCTTGGAGAGATAGAGACTACTTTGTAGCTAAG 2200
 Db 681 IleLeuSerAlaAlaPheCysGlnLeuPheGlyArgAspArgAspTyrPheValAlaLys 700
 QY 2201 AATCAAGGTACAGTACGAGGAACCTCTATTACGAGCACACGAAACCTATATCTCT 2260
 Db 701 AsnGlnGlyThrValTyrGlyGlyThrLeuTyrTyrGlnHisAsnGluThrTyrIleSer 720
 QY 2261 CTTCTTGGAACTACGCGCTTGTCTGTCTATGTTCTTACAGAGATCTCTGTTCTC 2320
 Db 721 LeuProCysLysLeuArgProCysSerLeuSerTyrValProThrGluIleProValLeu 740
 QY 2321 TTTTTCAGGAACCTTAGCTACCCATACCGATACGATCTGAAACCAAGTATACAACA 2380
 Db 741 PheSerGlyAsnLeuSerTyrThrHisThrAspAsnAspLeuLysThrLysTyrThrThr 760
 QY 2381 TATCTCTACTGTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGAAGA 2440
 Db 761 TyrProThrValLysGlySerTyrGlyAsnAspSerPheAlaLeuGluPheGlyGlyArg 780
 QY 2441 GCTCCGATTTGCTTAGTGAAGTCTCTATTGAGCAGTACATGCCCTTCATGAATTG 2500
 Db 781 AlaProIleCysLeuAspGluSerAlaLeuPheGluGlnTyrMetProPheMetLysLeu 800
 QY 2501 CAGTTTCTCTATGCATCAGGAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTT 2560
 Db 801 GlnPheValTyrAlaHisGlnGluGlyPheLysGluGlnGlyThrGluAlaArgGluPhe 820
 QY 2561 GGAAGTAGCGCTCTGTGAATCTTTCCTTACCTATCCGATCCGATTTGATGAAGATCA 2620
 Db 821 GlySerSerArgLeuValAsnLeuAlaLeuProIleGlyIleArgPheAspLysGluSer 840
 QY 2621 GACTGCCAAGATGCAAGTACAACTAACTCTGGTTATCTGTTGATCTGTTGATCTGTTGAT 2680
 Db 841 AspCysGlnAspAlaThrTyrAsnLeuThrLeuGlyTyrThrValAspLeuValArgSer 860
 QY 2681 AACCCGACTGTAGCAGCAACACTCGGAATAGCGGTGATCTTGGAAAACTTCGGTAGC 2740
 Db 861 AsnProAspCysThrThrThrLeuArgIleSerGlyAspSerThrLysThrPheGlyThr 880
 QY 2741 AATTGGCAAGACAGCTTTAGTCTCTCGTGCAGGAACCAATTTTCTTTAACTCAAT 2800
 Db 881 AsnLeuAlaArgGlnAlaLeuValLeuArgAlaGlyAsnHisPheCysPheAsnSerAsn 900
 QY 2801 TTTCAAGCCCTTAGCCAAATTTCTTTTGAATTCGTTGCTGCTCATCTCGCAATTACAATGA 2860
 Db 901 PheGluAlaPheSerGlnPheSerPheGluLeuArgGlySerSerArgAsnTyrAsnVal 920
 QY 2861 GACTTAGGAGCAAAATACCAATTC 2884
 Db 921 AspLeuGlyAlaLysTyrGlnPhe 928

RESULT 3
 ABB90535
 ID ABB90535 standard; Protein; 746 AA.
 XX
 AC ABB90535;
 XX
 DT 29-JUL-2002 (first entry)
 XX
 DE Chlamydia pneumoniae cp0015 protein, SEQ ID NO:19.
 XX
 KW Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
 KW human respiratory disease; cardiovascular disease; atherosclerosis;
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
 KW strain CWL029.
 XX

OS Chlamydia pneumoniae.
 XX WO200202606-A2.
 XX 10-JAN-2002.
 XX 03-JUL-2001; 2001WO-IB01445.
 XX 03-JUL-2000; 2000GB-0016363.
 PR 11-JUL-2000; 2000GB-0017047.
 PR 21-JUL-2000; 2000GB-0017983.
 PR 07-AUG-2000; 2000GB-0019368.
 PR 18-AUG-2000; 2000GB-0020440.
 PR 14-SEP-2000; 2000GB-0022583.
 PR 10-NOV-2000; 2000GB-0027549.
 PR 22-DEC-2000; 2000GB-0031706.
 XX (CHIR-) CHIRON SPA.
 PA Ratti G, Grandi G;
 PI WPI; 2002-154726/20.
 XX N-PSDB; ABU91193.
 DR
 DR
 XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes -
 XX Claim 1; Page 49-50; 364pp; English.
 PS
 XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is
 CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention
 CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed Chlamydia pneumoniae protein of the invention.
 XX
 SQ Sequence 746 AA;
 Alignment Scores:
 Pred. No.: 1.71e-309 Length: 746
 Score: 385.00 Matches: 746
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 71.45% Indels: 0
 DB: 23 Gaps: 0
 US-09-428-122-1 (1-3000) x ABB90535 (1-746)
 QY 647 ATGTGAGCTGTGTTTCTGAAATACCTCTCAAGAAAGCGGAGCCATTGAGACTTC 705
 Db 1 MetSerAlaLeuPheSerGluAsnThrSerSerLysLysGlyGlyAlaIleGlnThrSer 20
 QY 707 GATGCCCTTACCTACTGGAACCAAGGGAAGTCTCTTTTCTGACAATCTCTTCG 766
 Db 21 AspAlaLeuThrIleThrGlyAsnGlnGlyGluValSerPheSerAspAsnThrSerSer 40
 QY 767 GATTCTGAGCTCAATTTTACAGAGCTCGGTGACTATTTCTAATAATGCTAAAGTT 826
 Db 41 AspSerGlyAlaAlaIlePheThrGluAlaSerValThrIleSerAsnAsnAlaLysVal 60
 QY 827 TCCTTTATTGACAATAAGGTACAGGAGCGAGTCTCTCAACACGGGGATATGTCAGGA 886

Db 61 SerPheIleAspAsnLysValThrGlyAlaSerSerThrThrGlyAspMetSerGly 80
 QY 887 GGTGCTATCTGTCTTATAAACTAGTACAGATACTAAGGTACACCTCCTACTGGAATACAG 946
 Db 81 GlyAlaIleCysAlaYrLysThrSerThrAspThrLysValThrLeuThrGlyAsnGln 100
 QY 947 ATGTTACTCTTACGCAACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAGAAG 1006
 Db 101 MetLeuLeuPheSerAsnAsnThrSerThrAlaGlyGlyAlaIleYrValLysLys 120
 QY 1007 CTGCAACTGCTCCGAGGAGCACTTACCCTATTCCAGTAGAAATAGTCTCAATGAGGTACA 1066
 Db 121 LeuGluLeuAlaSerGlyGlyLeuThrLeuPheSerArgAsnSerValAsnGlyGlyThr 140
 QY 1067 GCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAAATGAGTTTATCCGCCGAT 1126
 Db 141 AlaProLysGlyGlyAlaIleAlaIleGluAspSerGlyGluLeuSerLeuSerAlaAsp 160
 QY 1127 AGTGCTGACATCTGCTTTTGGGAAATACAGTCACTTACTACTCTCTGGGAGGATAGA 1186
 Db 161 SerGlyAspIleValPheLeuGlyAsnThrValThrSerThrThrProGlyThrAsnArg 180
 QY 1187 AGTAGTATCGACTTAGGAACGAGTGCAGAGATGACAGCTTTGGTTCCTGCTGTGTAGA 1246
 Db 181 SerSerIleAspLeuGlyThrSerAlaLysMetThrAlaLeuArgSerAlaAlaGlyArg 200
 QY 1247 GCATCTACTCTATGATCCATAACTACAGAGATCATCCACACAGTTACAGATGCTTA 1306
 Db 201 AlaIleYrPheYrAspProIleThrThrGlySerSerThrThrValThrAspValLeu 220
 QY 1307 AAAGTTAATGAGACTCCGGCAGATTCTGCATCAATATACAGGGAACATCATCTTCACA 1366
 Db 221 LysValAsnGluThrProAlaAspSerAlaLeuGlnYrThrGlyAsnIleIlePheThr 240
 QY 1367 GGAGAAAGTTATCAGAGACAGAGCGCGAGATCTATAAATCTTACTTCGAGCTACTA 1426
 Db 241 GlyGluLysLeuSerGluThrGluAlaAlaAspSerLysAsnLeuThrSerLysLeuLeu 260
 QY 1427 CAGCCTGTAATCTTTTCAGGAGGTACTCTATCTTTAAACATGAGTACTGTCAGACT 1486
 Db 261 GlnProValThrLeuSerGlyGlyThrLeuSerLeuLysHisGlyValThrLeuGlnThr 280
 QY 1487 CAGGCATCTCACTCAACAGGAGATTCTCGTCTCGAAATGAGCTAGAGAACTACTCTAGAA 1546
 Db 281 GlnAlaPheThrGlnGlnAlaAspSerArgLeuGluMetAspValGlyThrThrLeuGlu 300
 QY 1547 CCTGCTGATACGACCATTAACAATTGCTGCTATTACATCAGTTCTATAGACGCTGCA 1606
 Db 301 ProAlaAspThrSerThrIleAsnAsnLeuValIleAsnIleSerSerIleAspGlyAla 320
 QY 1607 AAGAAGCAAAATAGAAACCAAGCTACGTCMAAAATCTGACTTTATCTGGAACCATC 1666
 Db 321 LysLysAlaLysIleGluThrLysAlaThrSerLysAsnLeuThrLeuSerGlyThrIle 340
 QY 1667 ACTTATATGACCGACCGCAGCTTTTATGAAATCATAGTTTAAAGAACTCTCAGTCC 1726
 Db 341 ThrLeuLeuAspProThrGlyThrPheYrGluAsnHisSerLeuArgAsnProGlnSer 360
 QY 1727 TACGACATCTTAGAGCTCAAGCTTCTGGAACCTGTAAACAGACCGCAGTACTCCAGAT 1786
 Db 361 TyrAspIleLeuGluLeuLysAlaSerGlyThrValThrSerThrAlaValThrProAsp 380
 QY 1787 CCTAATATGGGTGAGAAATCCATACGGCTATCAGGAACTTGGGCCCAATGTTTGG 1846
 Db 381 ProIleMetGlyGluLysPheHisYrGlyYrGlnGlyThrTrpGlyProIleValTrp 400
 QY 1847 GGGACAGGGCTTCTAGCTGCAACCTTCACTGAGCTTAAACTGGCTATATTCCTAAT 1906
 Db 401 GlyThrGlyAlaSerThrThrAlaThrPheAsnTrpThrLysThrGlyYrIleProAsn 420
 QY 1907 CCCGAGGCTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATTAGC 1966
 Db 421 ProGluArgIleGlySerLeuValProAsnSerLeuTrpAsnAlaPheIleAspIleSer 440

QY 1967 TCTCTCCATTATCTTATGAGACTGCAAAAGGGTTGCAGGAGACCGTCTGTTTTGG 2026
 Db 441 SerLeuHisYrLeuMetGluThrAlaAsnGluGlyLeuGlnGlyAspArgAlaPheTrp 460
 QY 2027 TGTCTCGATTATCTAATCTTCTCCATAAGGATAGTACAAAACACGACGCGGTTCCG 2086
 Db 461 CysAlaGlyLeuSerAsnPhePheHisLysAspSerThrLysThrArgArgGlyPheArg 480
 QY 2087 CATTTGAGTGGCGGTTATGTCTAGAGAGAAACCTACATCTTGTTCAGATAGATTCCT 2146
 Db 481 HisLeuSerGlyGlyYrValIleGlyGlyAsnLeuHisThrCysSerAspLysIleLeu 500
 QY 2147 AGTCTCGATTTCTGCTAGCTCTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAATCAA 2206
 Db 501 SerAlaAlaPheCysGlnLeuPheGlyArgAspArgAspTyrPheValAlaLysAsnGln 520
 QY 2207 GGTACAGTCTACGGAGGAACTCTCTATTACCAGACACAGAAACCTATATCTCTCTCT 2266
 Db 521 GlyThrValYrGlyGlyThrLeuYrYrGlnHisAsnGluThrTyrlleSerLeuPro 540
 QY 2267 TGCAAACTACGGCCTTCTTCTGTTCTTATGTCTCTACAGAGATTCCTGTTCTCTTTCA 2326
 Db 541 CysLysLeuArgProCysSerLeuSerYrValProThrGluIleProValLeuPheSer 560
 QY 2327 GGAAACCTTAGCTACACCCATACGATAACGATCTCGAATCAACCAAGTATACACATATCCT 2386
 Db 561 GlyAsnLeuSerYrThrHisThrAspAsnAspLeuLysThrLysYrThrThrYrPro 580
 QY 2387 ACTGTTAAAGGAAGCTGGGGAAATGATAGTTTCGCTTTAGAAATTCGGTGAAGAGCTCCG 2446
 Db 581 ThrValLysGlySerTrpGlyAsnAspSerPheAlaLeuGluPheGlyGlyAlaPro 600
 QY 2447 ATTTGCTTAGTGAAGTCTCTATTTGACGAGTACATGCCCTTCATGAAATTCGAGTTT 2506
 Db 601 IleCysLeuAspGluSerAlaLeuPheGluGlnYrMetProPheMetLysLeuGlnPhe 620
 QY 2507 GTCATATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGAAAGCTCGTGAATTTGGAAGT 2566
 Db 621 ValYrAlaHisGlnGluGlyPheLysGluGlnGlyThrGluAlaArgGluPheGlySer 640
 QY 2567 AGCGTCTGTGAACTTCTGCTTACCTATCGGATCGGATTTGATAGGAATCAGACTGC 2626
 Db 641 SerArgLeuValAsnLeuAlaLeuProIleGlyIleArgPheAspLysGluSerAspCys 660
 QY 2627 CAAGATGCAACGTACATCTAACTCTTGGTTATACCTGTCGATCTTGTCTAGTACCC 2686
 Db 661 GlnAspAlaThrYrAsnLeuThrLeuGlyYrThrValAspLeuValArgSerAsnPro 680
 QY 2687 GACTGTACGACAAACACTGCGAATTAGCGGTGATTTCTTTGAAAAACCTTCGTAAGATTTG 2746
 Db 681 AspCysThrThrThrLeuArgIleSerGlyAspSerTrpLysThrPheGlyThrAsnLeu 700
 QY 2747 GCAAGACAGAGCTTAGTCTTCGTCGAGGGAACCATTTTGTCTTAACCAATTTTGA 2806
 Db 701 AlaArgGlnAlaLeuValLeuArgAlaGlyAsnHisPheCysPheAsnSerAsnPheGlu 720
 QY 2807 GCCTTTAGCCAAATTTCTTTTGAATTCGCTGGGTCTATCTCGCAATTCATAGTACTTA 2866
 Db 721 AlaPheSerGlnPheSerPheGluLeuArgGlySerSerArgAsnYrAsnValAspLeu 740
 QY 2867 GGAGCAAAATACCAATTC 2884
 Db 741 GlyAlaLysYrGlnPhe 746

RESULT 4

AAY34611
 ID AAY34611 standard; Protein; 597 AA.
 AC AAY34611;
 XX
 DT 13-SEP-1999 (first entry)
 XX

Chlamydia pneumoniae transmembrane protein sequence.

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.

Chlamydia pneumoniae.

WO9927105-A2.

03-JUN-1999.

20-NOV-1998; 98WO-IB01890.

04-NOV-1998; 98US-0107078.

21-NOV-1997; 97FR-0014673.

(GEST) GENSET.

Griffais R;

WPI; 1999-357842/30.

Genome sequence of Chlamydia pneumoniae

Page 632-633; Disclosure; 1912pp; English.

AAV34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotide sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.

Sequence 597 AA;

Alignment Scores:
Pred. No.: 4,85e-238 Length: 597
Score: 2997.00 Matches: 596
Percent Similarity: 99.67% Conservative: 0
Best Local Similarity: 99.67% Mismatches: 1
Query Match: 55.41% Indels: 2
DB: 20 Gaps: 0

US-09-428-122-1 (1-3000) x AAY34611 (1-597)

| | | | |
|----|-----|---|-----|
| QY | 544 | CTTGAGTTTGACAAAAATGTCAGTTTGCTCTTCAGCAAAAATCTTTCAACGGATATCG | 603 |
| Db | 1 | LeuGluPheAsp-LysAsnValSerLeuLeuPheSerLysAsnPheSerThrAspAsnG | 20 |
| QY | 604 | CGGTGCTATCACGCAAAATCTTTCATTAACAGGACTACAAATGTCAGCTCTGTTTC | 663 |
| Db | 20 | YGIYAlaIleThrAlaLysThrLeuSerLeuThrGlyThrMetSerAlaLeuPheSe | 40 |
| QY | 664 | TGAATAATCTCTCAAGAAAGCGGAGCCATTACAGCTTCGATGCCCTTACCATTAC | 723 |
| Db | 40 | rGluAsnThrSerSerLysGlyGlyAlaIleGlnThrSerAspAlaLeuThrIleth | 60 |
| QY | 724 | TGAAACCAAGGGGAAGTCTCTTTTCTGCAATATCTTTCGGAATCTGGAGCTGCAAT | 783 |
| Db | 60 | rGlyAsnGlnGlyValSerPheSerAspAsnThrSerSerAspSerGlyAlaIle | 80 |
| QY | 784 | TTTTTACAGAGCCTCGGTGACTATTTCTAAATGCTAAAGTTTCTTATTTGACATAAA | 843 |
| Db | 80 | ePheThrGluAlaSerValThrIleSerAsnAlaLysValSerPheIleAspAsnLy | 100 |
| QY | 844 | GGTCAGAGGCGAGCTCTCAACACGGGGATATGTCAGGAGGTCTATCTGCTTA | 903 |

| | | | |
|----|------|--|------|
| Db | 100 | sValThrGlyAlaSerSerThrThrGlyAspMetSerGlyGlyAlaIleCysAlaTy | 120 |
| QY | 904 | TAAACTAGTACAGATTAAGTCAACCTCAGTGGAAATCAGATGTTACTTTCACAA | 963 |
| Db | 120 | rLysThrSerThrAspThrLysValThrLeuThrGlyAsnGlnMetLeuLeuPheSerAs | 140 |
| QY | 964 | CAATACATCACAAACAGCGGAGGAGCTATCTATGTGAAAAAGCTCGAAGCTTCGG | 1023 |
| Db | 140 | nasnThrSerThrThrAlaGlyGlyAlaIleTyValLysLysLeuGluLeuAlaSerGl | 160 |
| QY | 1024 | AGGACTTACCCCTATTCAGTAGAAATAGTCAATGGAGGTACAGCTCTCTAAAGTGGAGC | 1083 |
| Db | 160 | yGlyLeuThrLeuPheSerArgAsnSerValAsnGlyGlyThrAlaProLysGlyAl | 180 |
| QY | 1084 | CATAGCTATCGAAGATAGTGGGAATTGAGTTTATCCCGATAGTGTGACATTGTCTT | 1143 |
| Db | 180 | aileAlaIleGluAspSerGlyGluLeuSerLeuSerAlaAspSerGlyAspIleValPh | 200 |
| QY | 1144 | TTTAGGGAATACAGTCACTTCTACTCTCTGGGACGAATAGAGTAGTATCGACTTAGG | 1203 |
| Db | 200 | eLeuGlyAsnThrValThrSerThrThrProGlyThrAsnArgSerSerIleAspLeuGl | 220 |
| QY | 1204 | AACGAGTCAAAAGATGACAGCTTTGCGTTCTGCTGCTAGAGCCATCTACTTATGA | 1263 |
| Db | 220 | yThrSerAlaLysMetThrAlaLeuArgSerAlaAlaGlyArgAlaIleTyPheTyAs | 240 |
| QY | 1264 | TCCATTAACACTACAGATCATCCACAACAGTTACAGATGTTTAAAGTTAATGAGACTCC | 1323 |
| Db | 240 | pProIleThrThrGlySerSerThrThrValThrAspValLeuLysValAsnGluThrPr | 260 |
| QY | 1324 | GGCAGATTCTGCATCAATATACAGGGAACATCATCTTTCACAGGAGAAAAAGTTATCAGA | 1383 |
| Db | 260 | calaAspSerAlaLeuGlnTyThrGlyAsnIleIlePheThrGlyGluLysLeuSerGl | 280 |
| QY | 1384 | GACAGAGCCGCGAGATTCTAAAATCTTACTTTCGAGCTACTACAGCTGTAACTCTTTC | 1443 |
| Db | 280 | uThrGluAlaAlaAspSerLysAsnLeuThrSerLysLeuLeuGlnProValThrLeuSe | 300 |
| QY | 1444 | AGGAGTACTCTCTTTAAACATGGAGTCACTCTGCAGACTCAGGACTTCACTCAACA | 1503 |
| Db | 300 | rglyGlyThrLeuSerLeuLysHisGlyValThrLeuGlnThrGlnAlaPheThrGlnGl | 320 |
| QY | 1504 | GGCAGATTCTCGTCTCGAAATGGAGTAGGAATCTCTAGAACCTGTGTACTTAGCAC | 1563 |
| Db | 320 | nAlaAspSerArgLeuGluMetAspValGlyThrThrLeuGluProAlaAspThrSerTh | 340 |
| QY | 1564 | CATAACAATTTGGTCATTAAACATCAGTTCTATAGACGGTGCAGAGAGGCAAAATAGA | 1623 |
| Db | 340 | rileAsnAsnLeuValIleAsnIleSerSerIleAspGlyAlaLysLysAlaLysIleGl | 360 |
| QY | 1624 | AACCAAGCTAGCTCAAAAATCTGACTTTATCTGGAACCATCAGTTTATTCGACCCGAC | 1683 |
| Db | 360 | uThrLysAlaThrSerLysAsnLeuThrLeuSerGlyThrIleThrLeuLeuAspProth | 380 |
| QY | 1684 | GGGCGAGTTTATGAAATCATAGTTTAAAGAAATCTCAGTCTCTACGACATCTTAGAGCT | 1743 |
| Db | 380 | rglyThrPheTyThrGluAsnHisSerLeuArgAsnProGlnSerTyAspIleLeuGluLe | 400 |
| QY | 1744 | CAAAGCTCTGGAACCTGTAAACAAGCACCGAGTCCAGATCTCTATATATGGTGAGAA | 1803 |
| Db | 400 | uLysAlaSerGlyThrValThrSerThrAlaValThrProAspProIleMetGlyGluLy | 420 |
| QY | 1804 | ATTCCATTACGGCTATCAGGAACTTGGGGCCCAATTTGTTGGGACAGGGGCTCTAC | 1863 |
| Db | 420 | sPheHisTyGlyTyThrGlnGlyThrTrpGlyProIleValTrpGlyThrGlyAlaSerth | 440 |
| QY | 1864 | GACTGCAACTTCAACTGAGCTAAAATCGCTATATTTCTTAATCCCGAGGATCCGGCTC | 1923 |
| Db | 440 | rThrAlaThrPheAsnTrpThrLysThrGlyTyThrIleProAsnProGluArgIleGlyse | 460 |
| QY | 1924 | TTTAGTCCCTTAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCTCATTTATTTAT | 1983 |
| Db | 460 | rLeuValProAsnSerLeuTrpAsnAlaPheIleAspIleSerSerLeuHisTyLeuMe | 480 |

[illegible]

| | | | |
|----|------|---|------|
| Db | 603 | AsnProGlnArgGlnGlyProLeuValProAsnSerLeuThrGlySerPheSerAspIle | 622 |
| Qy | 1964 | AGCTCTCTCCATTATCTATTGAGACATGCCAAACGAAAGGTTGCGAGGAGACCGTGCTTTT | 2023 |
| Db | 623 | GlnAlaIleGlnGlyValIleGluArgSerAlaLeuThrLeucCysSerAspArgGlyPhe | 642 |
| Qy | 2024 | TGGTGTCTCGGATATCTACTCTCTCCATAGATAGTACAAAACACGACCGGGTTT | 2083 |
| Db | 643 | TrpAlaAlaGlyValAlaAsnPheLeuAspLysAspLysGlyGluLysArgLysIle | 662 |
| Qy | 2084 | CGCATTTGAGTGGCGGTTATGTATAGGAGGAAACCTACATATCTGTTCCAGATAAGATT | 2143 |
| Db | 663 | ArgHisLysSerGlyGlyTyrAlaIleGlyAlaAlaGlnThrCysSerGluAenLeu | 682 |
| Qy | 2144 | CTTAGTCTCGATTTTGTCTAGCTCTTTGGGAAGAGATAGACACTACTTTGTAGCTAAGAT | 2203 |
| Db | 683 | IleSerPheAlaPheCysGlnLeuPheGlySerAspLysAspPheLeuValAlaLysAen | 702 |
| Qy | 2204 | CAAGGTACAGTCTACGGAGGAATCTCTATTACCAGCACAAACCTATATCTCTCTT | 2263 |
| Db | 703 | HisThrAspThrTyrAlaGlyAlaPheTyrIleGlnHis | 718 |
| Qy | 2264 | CGTTGCAAACTACGGCCCTTGTGCTGTCTATTATGTTCTCT | 2314 |
| Db | 719 | CysSerGlyPheIleGlyCysLeuLeuAspLysLeuProGlySerTrpSerHisLysPro | 738 |
| Qy | 2315 | GTTCTCTTTTCAGGAAACCTTAGCTACACCCATACGGATACGATCTGAAACCAACATAT | 2374 |
| Db | 739 | LeuValLeuGluGlnLeuAlaTyrSerHisValSerAsnAspLeuLysThrLysIle | 758 |
| Qy | 2375 | ACAACATATCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGGTTTCAATTCGGT | 2434 |
| Db | 759 | ThrAlaTyrProGluValLysGlySerTrpGlyAsnAsnAlaPheAsnMetMetLeuGly | 778 |
| Qy | 2435 | GGAAGAGCTCGGATTGCTTAGTGAAGTCTCTATTGAGCAGTACATGCCCTTCATG | 2494 |
| Db | 779 | AlaSerSerHisSerTyrProGluTyrLeuHisCysPheAspThrTyrAlaProTyrIle | 798 |
| Qy | 2495 | AAATTGCAAGTTTGTCTATGACATCAGAGAGTTTAAAGAACAGGAAACAGAGCTCGT | 2554 |
| Db | 799 | LysLeuAsnLeuThrTyrIleArgGlnAspSerPheSerGluLysGlyThrGluGlyArg | 818 |
| Qy | 2555 | GAATTTGGAAGTAGCCGCTTGTGAAATCTTGCTTACTATCGGGATCCGATTTGATAAG | 2614 |
| Db | 819 | SerPheAspAspSerAsnLeuPheAsnLeuSerLeuProIleGlyValLysPheGluLys | 838 |
| Qy | 2615 | GAATCAGACTCCCAAGATGCAACGTACAATCTAATCTCTGTTTATCTGTGGATCTTGTT | 2674 |
| Db | 839 | PheSerAspCysAsnAspPheSerTyrAspLeuThrLeuSerTyrValProAspLeuIle | 858 |
| Qy | 2675 | CGTAGTAACCCCGACTGTACGACAACTCGCAATTACCGGTGATCTTTGGAAACCTTC | 2734 |
| Db | 859 | ArgAsnAspProLysCysThrThrAlaLeuValIleSerGlyAlaSerTrpGluThrTyr | 878 |
| Qy | 2735 | GGTACGATTTGGCAAGCAGCTTAGTCTCTCGTCAGGAGACCACTTTTGGCTTAAC | 2794 |
| Db | 879 | AlaAsnAsnLeuAlaArgGlnAlaLeuGlnValArgAlaGlySerHisTyrAlaPheSer | 898 |
| Qy | 2795 | TCAAAATTTTGAAGCCTTTAGCCCAATTTTCTTTGAAATTCGGTGGGTCTATCTCGCAATTAC | 2854 |
| Db | 899 | ProMetPheGluValLeuGlyGlnPheValPheGluValArgGlySerSerArgIleTyr | 918 |
| Qy | 2855 | AATGTAGCTTAGAGCAAAAATACCAATTC | 2884 |
| Db | 919 | AsnValAspLeuGlyGlyLysPheGlnPhe | 928 |

RESULT 6
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ID ABB
XX
AC ABB
XX

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|----|------|---|------|
| QY | 1145 | TTAGGGAATACAGTCACTTCTACTACTCCT---GGGACGAATAGAAGTAGTAGTCGACTTAA | 1201 |
| DB | 344 | AsnGlyAsnAlaIleValAlaThrThrProGlnThrThrLysArgAsnSerIleAspIle | 363 |
| QY | 1202 | GGAAACAGTGCAAAGATGACAGCTTTTCGTTTCGTCTGGTAGAGCCATCTACTTCTAT | 1261 |
| DB | 364 | GlySerThrAlaLysIleThrAsnLeuArgAlaIleSerGlyHisSerIlePhePheThr | 383 |
| QY | 1262 | GATCCCAATACTACAGGATCATCCACAACAGTTTACAGATGTCCTTAAAGTTAATGAGACT | 1321 |
| DB | 384 | AspProIleThrAlaAsnThrAlaAlaAspSerThrAspThrLeuAsnLeuAsnLysAla | 403 |
| QY | 1322 | CCGGCAGATTCTGCACATPACAAATATACAGGAAACATCATCTTCACAGGAGAAAAGTTATCA | 1381 |
| DB | 404 | AspAlaGlyAsnSerThrAspTyrSerGlySerIleValPheSerGlyGluLysLeuSer | 423 |
| QY | 1382 | GAGACAGAGCGCGAGATTCCTAAATCTTACTTCGAAGTACTACAGCTGTAACTCTT | 1441 |
| DB | 424 | GluAspGluAlaLysValAlaAspAsnLeuThrSerThrLeuLysGlnProValThrLeu | 443 |
| QY | 1442 | TCAGGAGGTACTCTATCTTAAACATGGAGTGACTCTGCAGACTCAGGCATTCACCTCAA | 1501 |
| DB | 444 | ThrAlaGlyAsnLeuValLeuLysArgGlyValThrLeuAspThrLysGlyPheThrGln | 463 |
| QY | 1502 | CAGGCAGATTCTCTCTCGAAATGGACGTAGGAATCTCTAGAACCTGCT---GATACT | 1558 |
| DB | 464 | ThrAlaGlySerSerValIleMetAspAlaGlyThrThrLeuLysAlaSerThrGluGlu | 483 |
| QY | 1559 | AGCACCATAAACAAATTTGGTCATTAAACATCAGTTCTATAGACGGTCAAGAGAGGCCAAA | 1618 |
| DB | 484 | ValThrLeuThrGlyLeuSerIleProValAspSerLeuGlyGluGlyLysValVal | 503 |
| QY | 1619 | ATGAAACCAAGTACGTCGTAACAAATCTGACTTTATCTGGAACCATCACTTTATGCGAC | 1678 |
| DB | 504 | IleAlaAlaSerAlaAlaSerLysAsnValAlaLeuSerGlyProIleLeuLeuLeuAsp | 523 |
| QY | 1679 | CCGACGGGCACGTTTATGAAATCATAGTTTAAAGAAATCCTCAGTCCTCAGCATCTTAA | 1738 |
| DB | 524 | AsnGlnGlyAsnAlaTyrGluAsnHisAspLeuGlyLysThrGlnAspPheSerPheVal | 543 |
| QY | 1739 | GAGCTCAAAAGCTCTCGAATCTTAACAGCACCGCAGTGTACTCAGATCCTATAATGGGT | 1798 |
| DB | 544 | GlnLeuSerAlaLeuGlyThrAlaThrThrThrAspValProAlaValProThrValAla | 563 |
| QY | 1799 | GAGAAATCCATTACGGCTATCAGGAACTTGGGGCCCAATGTTTCG----- | 1846 |
| DB | 564 | ThrProThrHisTyrGlyTyrGlnGlyThrTrpGly---MetThrTrpValAspAspThr | 582 |
| QY | 1847 | --GGGACAGGGGCTCTACGACTGCAACCTTCAACTGGACATAAACTGGCTATATTCCT | 1903 |
| DB | 583 | AlaSerThrProLysThrLysThrAlaThrLeuAlaTrpThrAsnThrGlyTyrLeuPro | 602 |
| QY | 1904 | AATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATTT | 1963 |
| DB | 603 | AsnProGluArgGlnGlyProLeuValProAsnSerLeuTrpGlySerPheSerAspIle | 622 |
| QY | 1964 | AGCTCTCCATTATCTTATCGAGACTGCAACGAGGGTTGACGAGGACCGTCTCTTT | 2023 |
| DB | 623 | GlnAlaIleGlnGlyValIleGluArgSerAlaLeuThrLeuCysSerAspArgGlyPhe | 642 |
| QY | 2024 | TGGTGTCTGGATTATCTTAATCTCTCCATAGGATAGTACAAAACACAGCAGCGGGTTT | 2083 |
| DB | 643 | TrpAlaAlaGlyValAlaAsnPheLeuAspLysAspLysGlyGluLysArgLysTyr | 662 |
| QY | 2084 | CGCCATTTGAGTGGCGGTATGTCTATAGGAGAAACCTTACATACTTGTTCAGATAAGATT | 2143 |
| DB | 663 | ArgHisLysSerGlyGlyTyrAlaIleGlyGlyAlaAlaGlnThrCysSerGluAsnLeu | 682 |
| QY | 2144 | CTTAGTGTGCTATTGTTCAGTCTTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAAT | 2203 |
| DB | 683 | IleSerPheAlaPheCysGlnLeuPheGlySerAspLysAspPheLeuValAlaLysAsn | 702 |

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|----------|--|---|------|
| QY | 2204 | C A G G T T A C A G T C T A C G G A G G A A C T C T C T A T T A C C A G C A C A C G A A A C C T A T A T C T C T C T T | 2263 |
| Db | 703 | H i s T h r A s p T h r T y r A l a G l y A l a P h e T y r I l e G l n H i s | 718 |
| QY | 2264 | C C T T G C A A A C T A C G G C C T C G T T C G T T G C T T A T G T T C C T | 2314 |
| Db | 719 | C y s S e r G l y P h e I l e G l y C y s L e u L e u A s p L y s L e u P r o G l y S e r T r p S e r H i s L y P r o | 738 |
| QY | 2315 | G T T C T C T C T T T C A G G A A C C T T A G C T A C A C C C A T A C C G A T A A C G A T C T G A A A C C A A C G A T A T | 2374 |
| Db | 739 | L e u V a l l e u G l u G l y G l n L e u A l a T y r S e r H i s V a l S e r A s n A s p L e u L y s T h r L y s T y r | 758 |
| QY | 2375 | A C A C A T A T C T A C T G T T A A A G G A A G C T G G G G A A T C A T A T G T T C G T T C G T T A G A A T T C G G T | 2434 |
| Db | 759 | T h r A l a T y r P r o G l u V a l L y s G l y S e r T r p G l y A s n A s n A l a P h e A s n M e t M e t L e u G l y | 778 |
| QY | 2435 | G G A A G A G C T C C G A T T T C T T A G A T G A A A G T G C T C T A T T T C A G C A G T A C A T G C C C T T C A T G | 2494 |
| Db | 779 | A l a S e r S e r H i s S e r T y r P r o G l u T y r L e u H i s C y s P h e A s p T h r T y r A l a P r o T y r I l e | 798 |
| QY | 2495 | A A A T T G C A G T T T G T C T A T G C A C A T C A G A A A G T T T T A A G A A C A G G A A C A C A A G A G C T C G T | 2554 |
| Db | 799 | L y s L e u A s n L e u T h r T y r I l e A r g G l n A s p S e r P h e S e r G l u L y s G l y T h r G l u G l y A r g | 818 |
| QY | 2555 | G A A T T T G G A A G T A G C C G T C T T G A A T C T T G C C T T A C T A T C G G G A T C C G A T T T G A T A A G | 2614 |
| Db | 819 | S e r P h e A s p A s p S e r A s n L e u P h e A s n L e u S e r L e u P r o I l e G l y V a l L y s P h e G l u L y s | 838 |
| QY | 2615 | G A A T C A G A C T G C C A A G A T G C A A C G T C A A N T C T A C T C T T G T T A T A C T G T G G A T C T T G T T | 2674 |
| Db | 839 | P h e S e r A s p C y s A s n A s p P h e S e r T y r A s p L e u T h r L e u S e r T y r V a l P r o A s p L e u I l e | 858 |
| QY | 2675 | C G T A G T A A C C C C A C T C T A G C A C A C A C T G C G A A T T A G C G G T G A T T C T T G G A A A C C C T T C | 2733 |
| Db | 859 | A r g A s n A s p P r o L y s C y s T h r A l a L e u V a l l e S e r G l y A l a S e r T r p G l u T h r T y r | 878 |
| QY | 2735 | G G T A G A A T T T G G C A A G A C A G C T T T A G T C C T T C G T C A G G A A C C A T T T T T G C T T T A A C | 2794 |
| Db | 879 | A l a A s n A s n L e u A l a A r g G l n A l a L e u G l n V a l A r g A l a G l y S e r H i s T y r A l a P h e S e r | 898 |
| QY | 2795 | T C A A A T T T T G A A G C C T T T A G C C A A T T T C T T T T G A A T T G C G T G G T C A T C T C G A A T T A C | 2855 |
| Db | 899 | P r o M e t P h e G l u V a l L e u G l y G l n P h e V a l P h e G l u V a l A r g L y S e r A r g I l e T y r | 918 |
| QY | 2855 | A A T G T A G A C T T A G G A G C A A A A T A C A A T T C | 2884 |
| Db | 919 | A s n V a l A s p L e u G l y G l y L y s P h e G l n P h e | 928 |
| RESULT 7 | | | |
| AY90237 | | | |
| ID | AA90237 standard; Protein; 928 AA. | | |
| XX | AA90237; | | |
| AC | AA90237; | | |
| DT | 29-AUG-2000 (first entry) | | |
| XX | Chlamydia antigen CPN100635. | | |
| DE | | | |
| XX | | | |
| KW | Chlamydia antigen; diagnosis; infection; community acquired pneumonia; | | |
| XW | therapy; upper respiratory tract disease; bronchitis; sinusitis; | | |
| KW | asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma. | | |
| XX | Chlamydia pneumoniae. | | |
| OS | | | |
| XX | | | |
| FH | Key | Location/Qualifiers | |
| FT | Peptide | 1..43 | |
| FT | | /note= "signal peptide" | |
| FT | Protein | 44..928 | |
| FT | | /note= "mature CPN100635" | |
| XX | | | |
| FN | WO200032794-A2. | | |
| XX | | | |
| PD | 08-JUN-2000. | | |

XX PF 01-DEC-1999; 99WO-CA01147.
 XX PR 01-DEC-1998; 98US-0110339.
 XX PR 01-DEC-1998; 98US-0110340.
 XX PR 01-DEC-1998; 98US-0110427.
 XX PR 01-DEC-1998; 98US-0110428.
 XX PR 01-DEC-1998; 98US-0110438.
 XX PA (CONV-) CONNAUGHT LAB LTD.
 XX PI Murdin AD, Oomen RP, Wang J;
 XX DR WPI; 2000-412339/35.
 XX DR N-PSDB; AAA30849, AAA30850.
 XX Nucleic acids encoding polypeptide antigens from Chlamydia useful for
 PT preventing, diagnosing and treating diseases such as community acquired
 PT pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
 PT asthma -
 XX
 PS Claim 16; Fig 3; 174pp; English.
 XX This sequence is a Chlamydia antigen of the invention, designated
 CC CPN100635. The nucleic acids (and their complementary sequences) may be
 CC used as diagnostic agents for detecting the presence of nucleic acids
 CC encoding Chlamydia antigens in samples according to standard methods,
 CC and therefore, for diagnosing Chlamydia infections. For example, they may
 CC be used as primers and probes for diagnostic polymerase chain reaction
 CC (PCR) assays. Antisense sequences may be used to down regulate
 CC expression of the proteins and may be used to treat infections. The
 CC nucleic acids may also be used to produce the protein antigens they
 CC encode according to standard recombinant DNA methodologies. The
 CC proteins may then be used as antigens for the production of antibodies
 CC (i.e. as vaccines) for preventing infection by Chlamydia. The
 CC antibodies may also be used as diagnostic reagents for detecting
 CC infections. Chlamydia is a pathogen implicated in the development of
 CC (for example) community acquired pneumonia, upper respiratory tract
 CC disease (especially bronchitis and sinusitis, asthmatic bronchitis,
 CC adult-onset asthma and acute exacerbations of asthma in adults.
 XX
 SQ Sequence 928 AA;
 Alignment Scores:
 Pred. No.: 1,38e-157 Length: 928
 Score: 2021.00 Matches: 438
 Percent Similarity: 61.05% Conservative: 142
 Best Local Similarity: 46.11% Mismatches: 326
 Query Match: 37.36% Indels: 44
 DB: 21 Gaps: 20
 US-09-428-122-1 (1-3000) x AAY90237 (1-928)
 QY 101 ATCAAGCTCTCTTCCCAAGTTGTGATT---TCTACATTTGCTATTTC----- 148
 Db 1 MetLysSerGlnPheSerTrpLeuValLeuSerSerThrLeuAlaCysPheThrSerCys 20
 QY 149 CCTTTGCTATGATTGCTACCGAGACAGATTTTGGATTCAAGTCGAGTTTCGATGGGAAT 208
 Db 21 SerThrValPheAlaAlaThrAlaGluAsnIleGlyProSerAspSerPheAspGlySer 40
 QY 209 AAAAAAT---GGTAATTTTTCAGTTCGTGAGAGTCAGGAGATCTCTGGAACCTACCTA 265
 Db 41 ThrAsnThrGlyThrThrProLysAsnThr-----ThrThrGlyIleAspThr 58
 QY 266 TTTAAGGAATGTCATCTCTAGAAATATTCTCTGGAACAGGACAGCAATCAGAAAAGC 325
 Db 59 LeuThrGlyAspIleThrLeuGlnAsnLeu---GlyAspSerAlaAlaLeuThrLysGly 77
 QY 326 TGTTTTAAACACATCAAGGGGATTTGACTTTTCAGAGTAACCGGAACCTCTATTGTTTC 385
 Db 78 CysPheSerAspThrThrGluSerLeuSerPheAlaGlyLysGlyThrSerLeuSerPhe 97

QY 386 CAAACGGTGTGATCGAGGACTGTAGCAGGGGCTGCTGTTTAAACAGCAGCGTGTAGATAAA 445
 Db 98 LeuAsnIleLysSer---SerAlaGluGlyAlaAlaLeu---SerValThrThrAspLys 115
 QY 446 TCTACCACGTTTATAGGTTTCTTCGCTATCTTTTATTTCGCTCTCTGGAATTCGATA 505
 Db 116 AsnLeuSerLeuThrGlyPheSerSerLeuThrPheLeuAlaAlaProSerSerValIle 135
 QY 506 ACTACC-----GGCAAGAGCGGTAGTCTCTACGGGTAGCTTGAGTTGACAAA 559
 Db 136 ThrThrProSerGlyLysGlyAlaValLysCysGly---GlyAspLeuThrPheAspAsn 154
 QY 560 AATGTCTAGTTTGTCTTTCAGCAAAAATCTTTTCAACGGATAATGGCGTGTATCACCGCA 619
 Db 155 AsnGlyThrIleLeuPheLysGlnAspTyrCysGluGluAsnGlyGlyAlaIleSerThr 174
 QY 620 AAAACTTTTCTTAAACAGGACTACATGCTAGCTCTGTTTCTGAAATACCTCTCA 679
 Db 175 LysAsnLeuSerLeuLysAsnSerThrGlySerIleSerPheGluGlyAsnLysSerSer 194
 QY 680 -----AAGAAAGCGGAGCCATTTCAGACTTCCGATGCCCTTACCATTTCTGGAAC 730
 Db 195 AlaThrGlyLysLysGlyAlaIleCysAlaThrGlyThrValAspIleThrAsnAsn 214
 QY 731 CAAGGGGAAGTCTCTTTTCTGCAATPACTTCTTCGATTCTCGAGCTGCAATTTTACA 790
 Db 215 ThrAlaProThrLeuPheSerAsnAsnIleAlaGluAlaAlaGlyGlyAlaIleAsnSer 234
 QY 791 GAACCTCGGTGACTATTCTTAATATGCTAAAGTTTCCTTATTGACATTAAGTCACA 850
 Db 235 ThrGlyAsnCysThrIleThrGlyAsnThrSerLeuValPheSerGluAsnSerValThr 254
 QY 851 GGAGCGAGCTCTCAACAGCGGGGATATGTCAGAGGTGCTATCTGTCTTATAAAACT 910
 Db 255 -----AlaThrAlaGly-----AsnGlyGlyAlaLeu----- 263
 QY 911 AGTACAGATCTAAGGTCAACCTCACTGGAATCAGATGTTACTTCTTCAGCAACAATACA 970
 Db 264 SerGlyAspAlaAspValThrIleSerGlyAsnGlnSerValThrPheSerGlyAsnGln 283
 QY 971 TCGACAACAGCGGAGGAGCTATCTATGTGAAAAGCTCGAAGCTGGCTTC-----GGA 1024
 Db 284 AlaValAlaAsnGlyGlyAlaIleTyrAlaLysLysLeuThrLeuAlaSerGlyGlyGly 303
 QY 1025 GGACTTACCTTATTCAGTAGAAATAGTCTCAATGAGGTACAGCTCCTAAAGGTGGAGCC 1084
 Db 304 GlyGlyAsnProPheSerAsnAsnIleValGlnGlyThrThrAlaGlyAsnGlyGlyAla 323
 QY 1085 ATAGCTATCGAAGATAGTGGGAATGAGTTTATCCCGCATAGTGGTGACATTTCTTT 1144
 Db 324 IleSerIleLeuAlaAlaGlyGlyCysSerLeuPheSerGluAlaGlyAspHisTyrLeu 343
 QY 1145 TTAGGAATACAGTCACTTCTACTACTCTCT---GGGACGAATAGAGTAGTAGTACACTTA 1201
 Db 344 AsnGlyAsnAlaIleValAlaThrThrProGlnThrThrLysArgAsnSerIleAspIle 363
 QY 1202 GGAACGAGTGAAGATGACAGCTTTTGGCTTCTGCTGCTGTAGAGCCATCTTCTTCT 1261
 Db 364 GlySerThrGlyLysAspHisGluLeuArgAlaIleSerGlyHisSerIlePhePheTyr 383
 QY 1262 GATCCCATTAACATCAGGATCATCCACACAGTTACAGATGTCTTAAAGTTAATCAGACT 1321
 Db 384 AspProIleThrAlaAsnThrAlaAlaAspSerThrAspThrLeuAsnLeuAsnLysAla 403
 QY 1322 CGGCGAGATTCGACTACATAATATACAGGACATCATCTTCACAGGAGAAAGTTATCA 1381
 Db 404 AspAlaGlyAsnSerThrAspTyrSerGlySerIleValPheSerGlyGlyLysLeuSer 423
 QY 1382 GGACACAGCGCGCAGATTCTAAATCTTACTTCGAAGCTACTCAGCGCTCTTAATCTTT 1441
 Db 424 GluAspGluAlaLysValAlaAspAsnLeuThrSerThrLeuLysGlnProValThrLeu 443
 QY 1442 TCAGGAGGTACTCTATCTTTTAAACATGAGTCACTCTCGCACTCAGCACTCACTCAA 1501

Db 444 ThrAlaGlyAsnLeuValLeuLysArgGlyValThrLeuAspThrLysGlyPheThrGln 463
QY 1502 CAGCGAGATCTCGTCTCGAAATGGAGCTAGGAACCTCTAGAACCTGCT---GATACT 1558
Db 464 ThrAlaGlySerValIleMetAspAlaGlyThrThrLeuLysAlaSerThrGluGlu 483
QY 1559 AGCACCATAACAATTTGGTCATTAACTCAGTTCTATAGACGGTGCAGAAAGGCAAAA 1618
Db 484 ValThrLeuThrGlyLeuSerIleProValAspSerLeuGlyGluGlyLysValVal 503
QY 1619 ATGAAACCAAGCTAGCTCAAAAATCTGACTTATCTGGAACCATCATCTTATTGGAC 1678
Db 504 IleAlaAlaSerAlaAlaSerLysAsnValAlaLeuSerGlyProIleLeuLeuLeuAsp 523
QY 1679 CCGACGGGCACGTTTATGAAATCATAGTTTAAAGAAATCCTCAGTCTACGACATCTTA 1738
Db 524 AsnGlnGlyAsnAlaTyThrGluAsnHisAspLeuGlyLysThrGlnAspPheSerPheVal 543
QY 1739 GAGCTCAAACTTCTGGAACTGTAAACAGCACCGAGTGAATCCAGATCCATAATAGGGT 1798
Db 544 GlnLeuSerAlaLeuGlyThrAlaThrThrAspValProAlaValProThrValAla 563
QY 1799 GAGAAATTCATTACGGCTATCAGGGAATTTGGGCCCAATTGTTGG----- 1846
Db 564 ThrProThrHisTyThrGlyThrGlnGlyThrTrpGly---MetThrTrpValAspThr 582
QY 1847 ---GGGACAGGGGCTTACGACTGCAACCTTCAACTGGACTAACTGCTATATTCCT 1903
Db 583 AlaSerThrProLysThrLysThrAlaThrLeuAlaTrpThrAsnThrGlyTyThrLeuPro 602
QY 1904 AATCCGAGCGATPCGGCTCTTAGTCCCTTAATAGCTTATGGAATGCATTATAGATATT 1963
Db 603 AsnProGluArgGlnGlyProLeuValProAsnSerLeuTrpGlySerPheSerAspIle 622
QY 1964 AGCTCTCCATATCTTATGGAGCTGCAACAGGGTTCAGGAGACCGGCTCTTT 2023
Db 623 GlnAlaIleGlnGlyValIleGluArgSerAlaLeuThrLeuCysSerAspArgGlyPhe 642
QY 2024 TGGTGTCTGGATATCTAACTCTTCCATAAGGATAGTACAAAACACGACGCGGTTT 2083
Db 643 TrpAlaAlaGlyValAlaAsnPheLeuAspLysAspLysGlyGluLysArgLysTyrr 662
QY 2084 CGCCATTGATGGCGGTATGTGCATAGGAGAAACCTACATACCTGTTGAGTAAAGATT 2143
Db 663 ArgHisLysSerGlyGlyTyThrAlaIleGlyAlaAlaGlnThrCysSerGluAsnLeu 682
QY 2144 CTAGTCTGCATTTTGTCTAGCTCTTTGGAAGATAGAGACTACTTTGAGCTAAGAAAT 2203
Db 683 IleSerPheAlaPheCysGlnLeuPheGlySerAspLysAspPheLeuValAlaLysAsn 702
QY 2204 CAAGGTACAGTCTACGGAGGAACCTCTTATACAGCACACGAAACCTATATCTCTTT 2263
Db 703 HisThrAspThrTyThrAlaGlyAlaPheTyThrIleGlnHis-----IleThrGlu 718
QY 2264 CTTTGCAGAACTACGGCTGTGTTGTTTATGTTCTCT-----ACAGAGATTCTCT 2314
Db 719 CysSerGlyPheIleGlyCysLeuLeuAspLysLeuProGlySerThrSerHisLysPro 738
QY 2315 GTTCTCTTTTCAGAAACCTTAGCTACACCCATACCGATACGATCTGMAAACCAAGTAT 2374
Db 739 LeuValLeuGluGlnLeuAlaTyThrTrpGlyAsnAsnAlaPheAsnMetMetLeuGly 758
QY 2375 ACAACATCTCTACTGTTAAAGGAGCTGGGGGAATGATAGTTTCGCTTTTGAATTCGGT 2434
Db 759 ThrAlaTyProGluValLysGlySerTrpGlyAsnAsnAlaPheAsnMetMetLeuGly 778
QY 2435 GGAAGAGCTCCGATTTGCTTAGATGAAAGTCTTATTTAGACGAGTACATGCCCTTCATG 2494
Db 779 AlaSerSerHisSerTyProGluTyThrLeuHisCysPheAspThrTyThrAlaProTyThr 798
QY 2495 AAATTGCAGTTGCTATGACATCAGGAAGGTTTAAAGACAGGAGACAGGAGCTCGT 2554

Db 799 LysLeuAsnLeuThrTyThrIleArgGlnAspSerPheSerGluLysGlyThrGluGlyArg 818
QY 2555 GAATTTGGAGTAGCGCTTGTGAATCTTGCTTACCTATCGGATCCGATTTGATAG 2614
Db 819 SerPheAspAspSerAsnLeuPheAsnLeuSerLeuProIleGlyValLysPheGluLys 838
QY 2615 GAATCAGACTGCCAAGATGCAACGTACATCTTAATCTCTGTTGTTATCTGCGATCTTGT 2674
Db 839 PheSerAspCysAsnAspPheSerTyAspLeuThrLeuSerTyValProAspLeuIle 858
QY 2675 CGTAGTAACCCGACTGTACGACAAACACATCGCAATTAGCGGTGATTTCTTGGAAACCTTC 2734
Db 859 ArgAsnAspProLysCysThrThrAlaLeuValIleSerGlyAlaSerTrpGluThrTy 878
QY 2735 GGTACGAATTTGGCAAGACAAGCTTTAGTCTCTTGTGCGAGGAAACCATTTTGTCTTTAAC 2794
Db 879 AlaAsnAsnLeuAlaArgGlnAlaLeuGlnValArgAlaGlySerHisTyThrAlaPheSer 898
QY 2795 TCATAATTTTGAAGCCCTTAGCCCAATTTCTTTGATTCGCTGGTGCATCTCGCAATTAC 2854
Db 899 ProMetPheGluValLeuGlyGlnPheValPheGluValArgGlySerSerArgIleTy 918
QY 2855 AATGTAGACTTAGGACGAAATAACCAATTC 2884
Db 919 AsnValAspLeuGlyGlyLysPheGlnPhe 928
RESULT 8
AAV69369
ID AAV69369 standard; Protein; 918 AA.
XX AAV69369;
AC AAV69369;
XX 19-JUN-2000 (first entry)
DT Amino acid sequence of the CPN100395 polypeptide.
XX CPN100395; Chlamydia infection; immune response; vaccine.
XX Chlamydia pneumoniae.
OS WO2000011183-A2.
XX 02-MAR-2000.
XX 18-AUG-1999; 99WO-IB01449.
XX 20-AUG-1998; 98US-0097187.
XX 20-AUG-1998; 98US-0097188.
XX 20-AUG-1998; 98US-0097189.
XX 20-AUG-1998; 98US-0097190.
XX 20-AUG-1998; 98US-0097195.
XX 20-AUG-1998; 98US-0097196.
XX 20-AUG-1998; 98US-0097197.
XX 27-AUG-1998; 98US-0097191.
XX 17-AUG-1999; 99US-0376770.
XX (CONN-) CONNAUGHT LAB LTD.
XX Murdin AD, Coenen RP;
XX WPI; 2000-224703/19.
XX N-PSDB; AAZ61509.
XX Novel antigens and corresponding DNA molecules that can be used to prevent, treat and diagnose disease caused by Chlamydia infection in mammals, especially humans -
XX Claim 19; Fig 15-E; 201pp; English.
XX AAV69362-69 represent Chlamydia pneumoniae polypeptides. The polypeptides are present in the bacterial membrane structure, in the external vicinity of the membrane structure, in the inclusion membrane structure, in the external vicinity of the inclusion membrane structure,
CC

CC and in the cytoplasm of the infected cell. The polypeptides may be
CC used to prevent, treat and detect the presence of Chlamydia infection
CC and/or the presence of Chlamydia in a sample. The polypeptides may
CC also be used to induce an immune response in a mammal. The vaccine
CC vector comprising the polynucleotides is used to induce an immune
CC response in a mammal. Antibodies directed against the polypeptides
CC may also be used therapeutically to treat and/or prevent a Chlamydia
CC infection.

| AA | Sequence | 918 AA; |
|----|----------|---------|
| SO | | |

| | | |
|------------------------|-----------|---------------|
| Alignment Scores: | | |
| Pred. No.: | 2,378-156 | Length: |
| Score: | 2006.00 | Matches: |
| Percent Similarity: | 61.39% | Conservative: |
| Best Local Similarity: | 45.57% | Mismatches: |
| Query Match: | 37.09% | Indels: |
| DB: | 21 | Gaps: |
| | | 20 |
| | | 918 |

US-09-428-122-1 (1-3000) x AAY69369 (1-918)

| | | | |
|----|-----|---|-----|
| Qy | 101 | ATGAAGTCTCTTCCCAAGTTGTATTTCTACATTGCTATTTCCCTTTGCTCTATG | 160 |
| Db | 1 | MetArgSerPheSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuMet | 20 |
| Qy | 161 | ATT-----GCTACCAGACAGTGTGGATTCAAGTCGCGAGTTTCATCGGAAT | 208 |
| Db | 21 | SerValSerAlaAspAlaAspLeuThrLeuGlySerArgAspSerTyrAsnGlyAsp | 40 |
| Qy | 209 | --AAAAATGGTAAATTTTCAGTTCGTGAGAGTCCAGGAAGATGCT---GGAACTACCTAC | 262 |
| Db | 41 | ThrSerThrThrGluPheThrProLysAlaAlaThrSerAspAlaSerGlyThrThrTyr | 60 |
| Qy | 263 | CTATTAAAGGAAATGTCACTCTAGAAATATTCCTGGACAGGACACGACATCACAAA | 322 |
| Db | 61 | IleLeuAspGlyAspValSerIleSerGln---AlaGlyLysGlnThrSerLeuThrThr | 79 |
| Qy | 323 | AGCTCTTTTAAACAACATPAGGCGGATTTGACTTTTCACAGGTAAACGGGAACCTCTCTATTG | 382 |
| Db | 80 | SerCysPheSerAsnThrAlaGlyAsnLeuThrPheLeuGlyAsnGlyPheSerLeuHis | 99 |
| Qy | 383 | TTCCAAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTGTTAAACAGCAGCGCTGTAGAT | 442 |
| Db | 100 | PheAspAsnIleIleSerSerThrValAlaGlyValValSerAsnThrAlaAlaSer | 119 |
| Qy | 443 | AAATCTACACGTTTATAGGGTTTTCTTCGCTATCTTTTATTGCTGCTCTCTCGAAGTTCG | 502 |
| Db | 120 | GlyIleThrLysPheSerGlyPheSerThrLeuArgMetLeuAlaAlaProArg----- | 137 |
| Qy | 503 | ATAACTACCGCAAGAGCGGTAGCTGCTCTACGGGTAGCTTGAGTTTGACAAAAAT | 562 |
| Db | 138 | ---ThrThrGlyLysGlyAlaIleLysIleThrAspGly---LeuValPheGluSerIle | 155 |
| Qy | 563 | GTCACTTTCCTCTTCAGCAAAAACCTTTTCAACCGGATAATGCGCGTGCTATCACCGCAAAA | 622 |
| Db | 156 | GlyAsnLeuAspLeuAsnGluAsnAlaSerSerGluAsnGlyGlyAlaIleAsnThrLys | 175 |
| Qy | 623 | ACTCTTTCAATAACAGGAGCTACAATGTCTAGCTCTGTTTCTGAAATATCTCTCTCAAG | 682 |
| Db | 176 | ThrLeuSerLeuThrGlySerThrArgPheValAlaPheLeuGlyAsnSerSerSerGln | 195 |
| Qy | 683 | AAAGCGGAGCCATTACAGACTCCGATGCCCTTACCATTACTGGAACCAAGGGAAGTC | 742 |
| Db | 196 | GlnGlyGlyAlaIleTyrAlaSerGlyAspSerValIleSerGluAsnAlaGlyIleLeu | 215 |
| Qy | 743 | TCCTTTTCTCAATACTCTTCGGATTCTTCGGAGTCCGAATTTTTCAGAAGCCTCGGTG | 802 |
| Db | 216 | SerPheGlyAsnAsnSerAlaThrThrSerGlyGlyAlaIleSerAlaGluGlyAsnLeu | 235 |
| Qy | 803 | ACTATTTCATAATGCTAAAGTTTCTTTTATTGACAATTAAGGTTCACAGAGCGAGTCC | 862 |
| Db | 236 | ValIleSerAsnAsnGlnAsnIlePhePheAspGlyCysLysAlaThr | 251 |

| | | | |
|------|----|---|------|
| 863 | QY | TCAACACGGGGATATGTCAGAGGTGCTACTGTGCTTTATAA-----ACTAGTACA | 916 |
| 252 | Db | -----ThrsnGlnGlyAlaIleAaspCysAsnLysAlaGlyAlaAsnPro | 266 |
| 917 | QY | GATACTAAGGTCAACCTCACTCGAATACAGATGTTACTCTTCAGCAACAATACATCGACA | 976 |
| 267 | Db | AspProIleuThrLeuSerGlyAsnGluSerLeuHisPheLeuAsnAsnThrAlaGly | 286 |
| 977 | QY | ACACGGGGAGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCGGGA---GGACTTACC | 1033 |
| 287 | Db | AsnSerGlyGlyAlaIleTyrThrLysLysLeuValLeuSerSerGlyArgGlyGlyVal | 306 |
| 1034 | QY | CTATTTCAGTAGAATAAGTGTCATCGAGGTACAGCTCTCTAAAGGTGGAGCCATAGCTATC | 1093 |
| 307 | Db | LeuPheSerAsnAsnLysAlaAlaAsnAlaThr---ProLysGlyGlyAlaIleAlaIle | 325 |
| 1094 | QY | GAAGATAGTGGGAAATTGAGTTTATCCGCGCATAGTGGTGACATGTCCTTTTACGGAAAT | 1153 |
| 326 | Db | LeuAspSerGlyGluIleSerIleSerAlaAaspLeuGlyAsnIleIlePheGluGlyAsn | 345 |
| 1154 | QY | ACAGTCACTTCTACTACT-----CCTGGGACGAATAGAAAGTAGTAGTATCGACTTAGGA | 1204 |
| 346 | Db | Thr---ThrSerThrThrGlySerProAlaSerValThrArgAsnAlaIleAaspLeuAla | 364 |
| 1205 | QY | ACGAGTCCAAAGATGACAGCTTTGCGTTCTGCTGCTGTAGAGCCATCTACTTCTATGAT | 1264 |
| 365 | Db | SerAsnAlalysPheLeuAsnLeuArgAlaThrArgGlyAsnLysValIlePheTyrAsp | 384 |
| 1265 | QY | CCCATACTACAGGATCATCCACACAGGTTCACAGATGCTCTTAAAGTTAATGAGACTCCG | 1324 |
| 385 | Db | ProIleThr-----SerSerGlyAlaThrAaspLysLeuSerLeuAsnLysAlaAasp | 401 |
| 1325 | QY | GCAGATTCTGCCTACATATACAGGGAACATCATCTTCCACGAGGAAAAAGTTATCAGAG | 1384 |
| 402 | Db | AlaGlySerGlyAsnThrTyrGluGlyTyrIleValPheSerGlyGluLysLeuSerGlu | 421 |
| 1385 | QY | ACAGAGCGCGAGATCTTAAATCTTACTTCGAGCTACTACAGCTGTAATCTCTTCA | 1444 |
| 422 | Db | GluGluLeuLysLysProAaspAsnLeuLysSerThrPheThrGlnAlaValGluLeuAla | 441 |
| 1445 | QY | GGAGGTACTCTATCTTTAAACATGGAGTGCATCTGCAGACTCAGGCATCTCACTCAACAG | 1504 |
| 442 | Db | AlaGlyAlaLeuValLeuLysAaspGlyValThrValValalalasnThrIleThrGlnVal | 461 |
| 1505 | QY | GCAGATTTCTGCTCGAAATGGAGCTAGGAACACTCTCTAGAA---CCTGCTGATCTAGC | 1561 |
| 462 | Db | GluGlySerLysValValMetAaspGlyGlyThrThrPheGluAlaSerAlaGluGlyVal | 481 |
| 1562 | QY | ACCATAAACAATTTGGTCATTAAACATCAGTCTCTATAGACGGTCAAGAGAGGCCAAATA | 1621 |
| 482 | Db | ThrLeuAsnGlyLeuAlaIleAsnIleAaspSerLeuAaspGlyThrAsnLysAlaIleIle | 501 |
| 1622 | QY | GAACCAAGCTAGCTCAAAAATCTGCATTTTACTCGAACCATCACTTTTATGGACCCG | 1681 |
| 502 | Db | LysAlaThrAlaAlaSerLysAaspValAlaLeuSerGlyProIleMetLeuValAaspAla | 521 |
| 1682 | QY | ACGGCAGCGTTTATGAAAAATCATAGTTTAAAGAAATCCTCAGTCTACGACATCTTAGAG | 1741 |
| 522 | Db | GlnGlyAsnTyrTyrGluHisAsnLeuSerGlnGlnGlnValPheProLeuIleGlu | 541 |
| 1742 | QY | CTCAAAGCTTCGAACTGTAAACAGACCCGAGTACTCAGATCTCTAATAATGGGTGAG | 1801 |
| 542 | Db | LeuSerAlaGlnGlyThrMetThrThrThrThrAspIleProAspThrProIleLeuAsnThr | 561 |
| 1802 | QY | AAATTCCATTACCGGTATCAGGGAACCTGGGGCCCAATTGTTGG-----GGGACA | 1852 |
| 562 | Db | ThrAsnHisTyrGlyTyrGlnGlyAsnTrpAsn---IleValTrpValAaspAaspAlaThr | 580 |
| 1853 | QY | GGGGCTCTCAGCTGCAACCTTCAACTCGGACTAAACCTGCGCTATATTCTTAATCCCGAG | 1912 |
| 581 | Db | AlaLysThrLysAsnAlaThrLeuThrThrThrLysThrGlyTyrLysProAsnProGlu | 600 |
| 1913 | QY | CGTATCGGCTTTTAGTCCCTAANTAGCTTATGGAAATGCATTTATAGATATTAGTCTCTC | 1972 |

Db 41 ThrSerThrThrGluPheThrProLysAlaAlaThrSerAspAlaSerGlyThrThrTyr 60
QY 263 CTAATTAAGGGAATGTCACCTCTAGAAATATTCCTGGACAGCACAGCAATCACAAA 322
Db 61 IleLeuAspGlyAspValSerIleSerGln---AlaGlyLysGlnThrSerLeuThrThr 79
QY 323 AGCTGTTTAAACACACTAAGGCGGATTGACTTTCACAGTAACGGGAATCTCTATTG 382
Db 80 SerCysPheSerAsnThrAlaGlyAsnLeuThrPheLeuGlyAsnGlyPheSerLeuHis 99
QY 383 TTCMAACGGTGGATGACGAGGACTCTACAGGGCTGCTGTTAACAGCAGCGTGTAGAT 442
Db 100 PheAsnIleIleSerSerThrValAlaGlyValValSerAsnThrAlaAlaSer 119
QY 443 AAATCTACACCTTTATAGGTTTCTCGCTATCTTTATTTAGTGGCTCTCTGGAAGTTTCG 502
Db 120 GlyIleThrLysPheSerGlyPheSerThrLeuArgMetLeuAlaAlaProArg----- 137
QY 503 ATAACCTACCGCAAGGAGCGGTTAGCTGCTCTACGGGTAGCTTG----- 547
Db 138---ThrThrGlyLysGlyAlaIleLysIleThrAspGlyLeuValPheGluSerIleGly 156
QY 548 AGTTTGACAAAATGTGAGTTGCTCTTCACCAAAAATCTTTCACGGAATAATCGCGGT 607
Db 157 AsnLeuAspGlnAsn-----GluAsnAlaSerSerGluAsnGlyGly 170
QY 608 GCTATCACCGCAAAAATCTTTCAATACAGGGACTACAATGCTAGCTGTGTTTCTGAA 667
Db 171 AlaIleAsnThrLysThrLeuSerLeuThrGlySerThrArgPheValAlaPheLeuGly 190
QY 668 AATACCTCTCAAGAAAGGCGGAGCATTCAGACTTCGGATGCCCTTACCATTACTGA 727
Db 191 AsnSerSerSerGlnGlnGlyGlyAlaIleTyrAlaSerGlyAspSerValIleSerGlu 210
QY 728 AACCAAGGGAAGTCTCTTTCTGACATACTCTCGATTCTGGAGCTGCAATTTT 787
Db 211 AsnAlaGlyIleLeuSerPheGlyAsnSerAlaThrThrSerGlyAlaIleSer 230
QY 788 ACAGAGCCTCGGTACTATTTCTAATAATGCTAAAGTTTCTCTTATTGACAAATAGGTC 847
Db 231 AlaGluGlyAsnLeuValIleSerAsnAsnGlnAsnIlePhePheAspGlyCysLysAla 250
QY 848 ACAGGAGCGAGCTCTCAACACGGGGATATGTCTAGGAGGTGCTATCTGCTGCTATAAA 907
Db 251 Thr-----ThrAsnGlyGlyAlaIleAspCysAsnLys 261
QY 908-----ACTAGTACAGATAAGTCAACCTCACTGGAAATCAGATGTTACTCTTCAGC 961
Db 262 AlaGlyAlaAsnProAspProIleLeuThrLeuSerGlyAsnGluSerLeuHisPheLeu 281
QY 962 AACATATACGCAACACAGCGGAGGAGCTATCTATGTGAAAGCTCGAATCGGCTTC 1021
Db 282 AsnAsnThrAlaGlyAsnSerGlyGlyAlaIleTyrThrLysLysLeuValLeuSerSer 301
QY 1022 GGA---GGACTTACCTATTTCAGTAGAATATGTCTCATGGAGGTACAGCTCTCAAGGT 1078
Db 302 GlyArgGlyGlyValLeuPheSerAsnAsnLysAlaAlaAsnAlaThr---ProLysGly 320
QY 1079 GGAGCCATAGCTATCGAAGATAGTGGGAATTCAGTTTATCCGCCGATAGTGGTGCATT 1138
Db 321 GlyAlaIleAlaIleLeuAspSerGlyGluIleSerIleSerAlaAspLeuGlyAsnIle 340
QY 1139 GTCTTTTTAGGAATACAGTCACTTCTACT-----CCTGGCAGCAATAGAGT 1189
Db 341 IlePheGluGlyAsnThr---ThrSerThrThrGlySerProAlaSerValThrArgAsn 359
QY 1190 AGTATCGACTTAGGAACGAGTGCAAGATGACAGCTTGTGCTGCTGCTGTAGAGCC 1249
Db 360 AlaIleAspLeuAlaSerAsnAlaLysPheLeuAsnLeuArgAlaThrArgGlyAsnLys 379
QY 1250 ATCTACTTCTATGATCCCAACTACAGGATCATCCACACAGTTACAGATGCTTAAAA 1309
Db 380 ValIlePheTyrAspProIleThr-----SerSerGlyAlaThrAspLysLeuSer 396

QY 1310 GTTAATGAGACTCGGCGAGATTCTGCACATACATATACAGGGAACATCATCTTCCACAGA 1369
Db 397 LeuAsnLysAlaAspAlaGlySerGlyAsnThrTyrGluGlyTyrIleValPheSerGly 416
QY 1370 GAAAGTTATCAGACAGAGCGCGCAGATTCTTAAATAATCTTACTTCGAAGCTACTACAG 1429
Db 417 GluLysLeuSerGluGluGluLeuLysLysProAspAsnLeuLysSerThrPheThrGln 436
QY 1430 CCTGTAACTCTTTCAGGAGGTACTCTATCTTTTAAAAATCATGAGTACTCTGACACTCAG 1489
Db 437 AlaValGluLeuAlaAlaGlyAlaLeuValLeuLysAspGlyValThrValValAlaAsn 456
QY 1490 GCATTCCTCAACAGGCGAGATTCTGCTCTCGAATTCGACGTAGCAACTACTCTAGAA--- 1546
Db 457 ThrIleThrGlnValGluGlySerLysValValMetAspGlyGlyThrThrPheGluAla 476
QY 1547 CTTCTCATACTAGCACCATAAACAATTTGCTCAATTAACATCATGTTCTATAGACGGTGCA 1606
Db 477 SerAlaGluGlyValThrLeuAsnGlyLeuAlaIleAsnIleAspSerLeuAspGlyThr 496
QY 1607 AAGAAGCAAAAATAGAAACCAAGCTACGTCAAAAATCTGACTTTATCTGGAACCATC 1666
Db 497 AsnLysAlaIleIleLysAlaThrAlaAlaSerLysAspValAlaLeuSerGlyProIle 516
QY 1667 ACTTTATTGACCCGCGGCGACGTTTATGAAAATCATAGTTTAAGAAATCCTCAGTCC 1726
Db 517 MetLeuValAspAlaGlnGlyAsnTyrTyrGluHisAsnLeuSerGlnGlnVal 536
QY 1727 TACGACATCTTACAGCTCMAAGCTTCTGMACTCTAACAGCACCGAGTCACTCCAGAT 1786
Db 537 PheProLeuIleGluLeuSerAlaGlnGlyThrMetThrThrThrAspIleProAspThr 556
QY 1787 CCTATAATGGGTGAGAAATTCATTTACGGCTATCAGGGAATCTGGGCCCAATGTTTGG 1846
Db 557 ProIleLeuAsnThrThrAsnHisTyrGlyTyrGlnGlyThr---GlyIleValTyr 575
QY 1847-----GGACAGGCGCTTCTACGACTCAACCTTCAACTGGACTTAAACCTGGCTAT 1897
Db 576 ValAspAlaThrAlaLysThrLysAsnAlaThrLeuThrThrLysThrGlyTyr 595
QY 1898 ATTCCTAATCCGAGCTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATA 1957
Db 596 LysProAsnProGluArgGlnGlyProLeuValProAsnSerLeuTyrGlySerPheVal 615
QY 1958 GATATTAGCTCTCTCCATTATCTTATGAGACTGCAACGAAGGTTGACGGGACCGT 2017
Db 616 AspValArgSerIleGlnSerLeuMetAspArgSerThrSerSerLeuSerSerThr 635
QY 2018 GCTTTTGTGTGCTGGATTATCTAATCTTCCATAGGATAGTACAAAAACACGACGC 2077
Db 636 AsnLeuTrpValSerGlyIleAlaAspPheLeuHisGluAspGlnLysGlyAsnGlnArg 655
QY 2078 GGGTTTCGCCATTTGAGTGGCGGTTATGTCTATGAGGAGAACTCATACTTTGTTCAAGT 2137
Db 656 SerTyrArgHisSerSerAlaGlyTyrAlaLeuGlyGlyGlyPhePheThrAlaSerGlu 675
QY 2138 AAGATTCTTAGTGTGCTGCTTTGTCAGCTCTTTGGAAGATAGAGACTACTTTAGCT 2197
Db 676 AsnPhePheAsnPheAlaPheCysGlnLeuPheGlyTyrAspLysAspHisLeuValAla 695
QY 2198 AAGATCAAGGTACAGTCTACGGGAACCTCTCTATTACAGCAC-----AACGAA 2248
Db 696 LysAsnHisThrHisValTyrAlaGlyAlaMetSerTyrArgHisLeuGlyGluSerLys 715
QY 2249 ACCTATATCTCTCTCTCTTCTGCAAACTACGGCCTTGTTCGTTCTTATGTTCTCTACAGAG 2308
Db 716 ThrLeuAlaLysIle-----LeuSerGlyAsnSerAspSer 727
QY 2309 ATTCTGTTCTCTTTTCAGGAAACCTTAGCTACACCCATACCGATTAACGATCTGAAACC 2368
Db 728 LeuProPheValPheAsnAlaArgPheAlaTyrGlyHisThrAspAsnAsnMetThrThr 747

QY 2369 AAGTATACACATATCTACTGTTAAAGGAGCTGGGGAATGATAGTTTCGTTAGTA 2428
 |||||
 Db 748 LysThrThrGlyThrSerProValLysGlySerTrpGlyAsnAspAlaPheGlyIleGlu 767
 |||||
 QY 2429 TTCGGTGGAGAGCTCCGATTTGCTTAGAT--GAAAGTGCTCTATTGACGAGTACATG 2485
 |||||
 Db 768 CysGlyGlyAlaIleProValValAlaSerGlyArgSerTrpValAspThrHisThr 787
 |||||
 QY 2486 CCTTCATGAATGAGTTTGTCTATGACATCAGGAAGGTTTAAAGAACAGGAACA 2545
 |||||
 Db 788 ProPheLeuAsnLeuGluMetIleTyrAlaHisGlnAsnAspPheLysGluAsnGlyThr 807
 |||||
 QY 2546 GAAGCTCGTGAATTCGAAGTACCGCTCTGTGAATCTTCCTTACCTATCGGATCCGA 2605
 |||||
 Db 808 GluGlyArgSerPheGlnSerGluAspLeuPheAsnLeuAlaValProValGlyIleLys 827
 |||||
 QY 2606 TTTGATGAAGGAATCAGATGCCAAGATGCAACGTACAACTCTTGTGTTATCTGTG 2665
 |||||
 Db 828 PheGluLysPheSerAsp-----LysSerThrTyrAspLeuSerIleAlaTyrValPro 845
 |||||
 QY 2666 GATCTTCTCGTAGTAACCCGACTGTACGACAACTGCGAATGACCGTGATCTTGG 2725
 |||||
 Db 846 AspValIleArgAsnAspProGlyCysThrThrThrLeuMetValSerGlyAspSerTrp 865
 |||||
 QY 2726 AAAACCTTCGTTAGCAATTTGGCAAGACAAGCTTTAGTCTCTGTCAGGGAACCATTT 2785
 |||||
 Db 866 SerThrCysGlyThrSerLeuSerArgGlnAlaLeuLeuValArgAlaGlyAsnHis 885
 |||||
 QY 2786 TGCTTTAACTCAAAATTTGAAGCCTTTAGCCAAATTTCTTTGAATTCGCGTCACT 2845
 |||||
 Db 886 AlaPheAlaSerAsnPheGluValPheSerGlnPheGluValGluLeuArgGlySerSer 905
 |||||
 QY 2846 CGCAATTAATGTAGACTTAGGAGCAAAATACCAATTC 2884
 |||||
 Db 906 ArgSerTyrAlaIleAspLeuGlyGlyArgPheGlyPhe 918
 |||||

RESULT 10
 AAW88429
 ID AAW88429 standard; Protein; 914 AA.
 XX
 AC AAW88429;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE Chlamydia pneumoniae surface exposed protein Omp5.
 XX
 KW Omp5; outer membrane protein 5; surface exposed protein; antigen;
 KW infection; diagnosis; vaccine; asthma; atherosclerosis; asthma.
 XX
 OS Chlamydia pneumoniae.
 XX
 PN W09858953-A2.
 XX
 PD 30-DEC-1998.
 XX
 DF 19-JUN-1998; 98WO-0000744.
 XX
 PR 23-JUN-1997; 97DK-0000744.
 XX
 PA (BIRK/) BIRKELUND S.
 PA (CHRI/) CHRISTIANSEN G.
 XX
 XX Birkelund S, Christiansen G, Knudsen K, Madesen A;
 PI Mygind P;
 XX
 XX WPI; 1999-105610/09.
 DR N-PSDB; AAX06828.
 DR
 XX
 XX Species-specific test for identifying mammals infected with
 PT Chlamydia pneumoniae - comprises detecting antibodies specific for
 PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
 PT these proteins

PS Disclosure; Page 78-80; 115pp; English.
 XX
 CC This polypeptide is described as a subsequence of the claimed
 CC novel surface exposed protein Omp5 (see AAW88418) of Chlamydia
 CC pneumoniae, a human respiratory pathogen. The invention provides
 CC a new species specific test for identifying mammals (including
 CC humans) infected with C. pneumoniae. The test comprises detecting
 CC antibodies specific for surface exposed proteins Omp4-Omp15 (see
 CC AAW88417-28) or detecting nucleic acid fragments encoding them (see
 CC AAX06816-27), especially by PCR. The proteins are also used in the
 CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids
 CC and proteins can also be used in the immunization of mammals, the
 CC nucleic acids being particularly useful as DNA vaccines for
 CC effecting in vivo expression of antigens. The vaccines may also
 CC prevent atherosclerosis and bronchial asthma, which are possibly
 CC associated with C. pneumoniae.
 XX
 SQ Sequence 914 AA;
 Alignment Scores:
 Pred. No.: 2,78e-155 Length: 914
 Score: 1993.00 Matches: 432
 Percent Similarity: 61.22% Conservative: 141
 Best Local Similarity: 46.15% Mismatches: 319
 Query Match: 36.85% Indels: 44
 DB: Gaps: 20
 US-09-428-122-1 (1-3000) x AAW88429 (1-914)
 QY 101 ATGAAGTCTTCTTCCCAAGTTTGTATT--TCTACATTTCTATTTC----- 148
 |||||
 Db 1 MetLysSerGlnPheSerTrpLeuValLeuSerSerThrLeuAlaCysPheThrSerCys 20
 |||||
 QY 149 CCTTGTCTATGATTGCTACCGAGACAGTTCGATTCAGTCGAGTTTCGATGGAAT 208
 |||||
 Db 21 SerThrValPheAlaAlaThrAlaGluAsnIleGlyProSerAspSerPheAspGlySer 40
 |||||
 QY 209 AAAAAT--GGTAATTTTTCAGTTCGTGAGAGTCAGGAGATCTGGAACCTACTACTTA 265
 |||||
 Db 41 ThrAsnThrGlyThrThrProLysAsnThr-----ThrThrGlyIleAspThr 58
 |||||
 QY 266 TTTAAGGGAAATGCTCACTTAGAAATATTTCTGGAACAGGACAGCAATCACAAAAGC 325
 |||||
 Db 59 LeuThrGlyAspIleThrLeuGlnAsnLeu--GlyAspSerAlaAlaLeuThrLysGly 77
 |||||
 QY 326 TGTTTAAACAACACTAAGCGGATTCGATTCACAGGTAAACGGAACTCTCTATTGTTTC 385
 |||||
 Db 78 CysPheSerAspThrThrGluSerLeuSerPheAlaGlyLysGlyTyrSerLeuSerPhe 97
 |||||
 QY 386 CAAACGGTGATCAGGAGCTGTAGCAGGGCTGTCTTAAACAGCAGCGGTGATAGAAA 445
 |||||
 Db 98 LeuAsnIleLysSer---SerAlaGluGlyAlaAlaLeu---SerValThrThrAspLys 115
 |||||
 QY 446 TCTACACGTTTATAGGGTTTCTCGCTATCTTTTATTCGCTCTCTCGAAGTTCGATA 505
 |||||
 Db 116 AsnLeuSerLeuThrGlyPheSerSerLeuThrPheLeuAlaAlaProSerSerValIle 135
 |||||
 QY 506 ACTACC-----GGCAAGAGCGGTTAGTCTCTACGGGTAGCTTGATTTGACAAAA 559
 |||||
 Db 136 ThrThrProSerGlyLysGlyAlaValLysCysGly---GlyAspLeuThrPheAspAsn 154
 |||||
 QY 560 AATGTCAGTTTGTCTTTCAGCAAAACTTTTCAACGGATAATGCGGTGCTATCACCGCA 619
 |||||
 Db 155 AsnGlyThrIleLeuPheLysGlnAspTyrCysGluGluAsnGlyAlaIleSerThr 174
 |||||
 QY 620 AAAACTCTTTCATTACAGGGACTACAAATGCTAGCTCTGTTTCTGAAAAATACCTCTCA 679
 |||||
 Db 175 LysAsnLeuSerLeuLysAsnSerThrGlySerIleSerPheGluGlyAsnLysSerSer 194
 |||||
 QY 680 -----AGAAAGCGGAGCGCAATTCAGACTTCGATCCGCTTACCATTTACTGGAAC 730
 |||||
 Db 195 AlaThrGlyLysLysGlyAlaIleCysAlaThrGlyThrValAspIleThrAsnAsn 214
 |||||

731 CAAGGGGAAGTCTCTTTCTTCTGACAACTACTCTTTCGGAATCTGAGCTGCAATTTTACA 790
 215 ThrAlaProThrLeuPheSerAsnAsnIleAlaGluAlaAlaGlyGlyAlaIleAsnSer 234
 791 GAAGCTCGGTGACTATTCTTAATAATGCTAAAGTTTCCTTTATTGACATAAGGTCACA 850
 235 ThrGlyAsnCysThrIleThrGlyAsnThrSerLeuValPheSerGlyAsnSerValThr 254
 851 GGACGGAGCTCCTCAACACGGGGATATGTCAGAGGTGCTATCTGTGCTTATAAAACT 910
 255 -----AlaThrAlaGly-----AsnGlyGlyAlaLeu----- 263
 911 AGTACAGATACTAAGGTCACCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATACA 970
 264 SerGlyAspAlaAspValThrIleSerGlyAsnGlnSerValThrPheSerGlyAsnGln 283
 971 TCGACAACAGCGGGAGGAGCTATCTATGTGAAGAAGCTCGAAGTGGCTTC-----GGA 1024
 284 AlaValAlaAsnGlyGlyAlaIleThrAlaLysLysLeuThrLeuAlaSerGlyGlyGly 303
 1025 GGACTTACCTTATTCAGTAGAAATAGTGTCAATGAGGTGAGGTCTCTTAAGGTGGAGCC 1084
 304 GlyGlyIleSerPheSerAsnAsnIleValGlnGlyThrThrAlaGlyAsnGlyGlyAla 323
 1085 ATAGCTATCGAAGATAGTGGGAATGAGTTTATCCGCGCATAGTGGTGACATTGCTTTT 1144
 324 IleSerIleLeuAlaAlaGlyGlyCysSerLeuSerAlaGluAlaGlyAspIleThrPhe 343
 1145 TTAGGAATACAGTCACTTCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1201
 344 AsnGlyAsnAlaIleValAlaThrThrProGlnThrThrLysArgAsnSerIleAspIle 363
 1202 GGAACGAGTGAAGATGACAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 1261
 364 GlySerThrAlaLysIleThrAsnLeuArgAlaIleSerGlyHisSerIlePheThr 383
 1262 GATCCCATTAACATACAGGATCCCAACACAGTTACAGATGCTTTAAAGTTTAATCAGACT 1321
 384 AspProIleThrAlaAsnThrAlaAlaAspSerThrAspThrLeuAsnLeuAsnLysAla 403
 1322 CCGGAGATTCGCTACTACAAATATACAGGAACATCATCTTCACAGGAGAAAGTTATCA 1381
 404 AspAlaGlyAsnSerThrAspThrSerGlySerIleValPheSerGlyGlnLysLeuSer 423
 1382 GAGACAGAGCGCGAGATTCTAAATCTTACTTCAAGCTACTACAGCTGTAATCTT 1441
 424 GluAspGluAlaLysValAlaAspAsnLeuThrSerThrLeuLysGlnProValThrLeu 443
 1442 TCAGGAGGTACTCTATCTTTTAAACATGAGGTGACTCTGAGACTCAGGATCAGCTCAA 1501
 444 ThrAlaGlyAsnLeuValLeuLysArgGlyValThrLeuAspThrLysGlyPheThrGln 463
 1502 CAGGCGAGATCTCGTTCGAAATGAGGTAGGAGTACTCTAGAACCTGCT---GATACT 1558
 464 ThrAlaGlySerSerValIleMetAspAlaGlyThrThrLeuLysAlaSerThrGluGlu 483
 1559 AGCACATAACAATTTGGTTCATTAACATCAGTTCTATAGACGGTGCACAGAGGCAAAA 1618
 484 ValThrLeuThrGlyLeuSerIleProValAspSerLeuGlyGluGlyLysLysValVal 503
 1619 ATAGAAACCAAGCTACGTCACAAATAATCTGACTTTATCTGGAAACCATCATTATTGGAC 1678
 504 IleAlaAlaSerAlaAlaSerLysAsnValAlaLeuSerGlyProIleLeuLeuLeuAsp 523
 1679 CCGAGCGGCGAGTTTATGAAATCATAGTTTAAAGATCTCTCAGTCTCAGCATCTTA 1738
 524 AsnGlnGlyAsnAlaThrGluAsnHisAspLeuGlyLysThrGlnAspPheSerPheVal 543
 1739 GAGCTCAAGGCTTCTGGAACCTGTAAACAGACAGCCAGCTGACTCCAGATCTCTATAATGGT 1798
 544 GlnLeuSerAlaLeuGlyThrAlaThrThrThrAspValProAlaValProThrValAla 563
 1799 GAGAAATTCCTATTACGGCTATACGGGAACCTTGGGGCCCAATTGTTTGG----- 1846

564 ThrProThrHisThrGlyThrGlnGlyThrTrpGly---MetThrTrpValAspAspThr 582
 1847 ---GGACACGGGCTTCTAGACTGCAACCTTCAACTGGAATAAACTGGCTATATTCCT 1903
 583 AlaserThrProLysThrLysThrAlaThrLeuAlaThrTrpThrAsnThrGlyThrLeuPro 602
 1904 AATCCCGAGCGTATCGCTCTTTAGTCCCTTAAGTCTTATGGAATGCAATTTATAGATATT 1963
 603 AsnProGlyArgGlnGlyProLeuValProAsnSerLeuTrpGlySerPheSerAspIle 622
 1964 AGCTCTCTCCATATTCTTATGAGACTGCAACGAAAGGTTGCAGGAGACCGTCTTTT 2023
 623 GluAlaIleGlnGlyValIleGluArgSerAlaLeuThrLeuCysSerAspArgGlyPhe 642
 2024 TGGTGTCTCGATTATCTTCTTCTTCCATAGGATAGTACAAAACACACACGGGGTTT 2083
 643 TrpAlaAlaGlyValAlaAsnPheLeuAspLysLysLysGlyGlyLysArgLysThr 662
 2084 CGCATTTGAGTGGCGGTATGTATAGGAGGAAACCTACATATCTTCTTCTCAGATAAGATT 2143
 663 ArgHisLysSerGlyGlyThrAlaIleGlyAlaAlaGlnThrCysSerGluAsnLeu 682
 2144 CTTAGTGTCTGATTCTTCTGAGCTCTTTGGAAGAGATAGACTACTTTGTAGCTTAAGAAT 2203
 683 IleSerPheAlaPheCysGlnLeuPheGlySerAspLysAspPheLeuValAlaLysAsn 702
 2204 CAAGGTACAGTCTACGAGGAGTCTCTTATCAGGACACACAACTATATCTCTCTT 2263
 703 HisThrAspThrThrAlaGlyAlaPheThrIleGlnHis-----IleThrGlu 718
 2264 CTTTGCAAACTACGGCTTGTCTGTTCTTATGTTCTCT-----ACAGAGATTCTT 2314
 719 CysSerGlyPheIleGlyCysLeuLeuAspLysLeuProGlySerThrSerHisLysPro 738
 2315 GTTCTCTTTTTCAGGAAACCTTAGCTACACCATACCGAATAACGATCGTGAACCAAGTAT 2374
 739 LeuValLeuGluGlyGlnLeuAlaThrSerHisValSerAsnAspLeuLysThrLysThr 758
 2375 ACAACATATCTTCTGTTTAAAGGAGCTGGGGATGATAGTCTTTCGCTTTAGATTCCGT 2434
 759 ThrAlaThrProGluValLysGlySerTrpGlyAsnAsnAlaPheAsnMetMetLeuGly 778
 2435 GGAAGAGTCCGATTGCTTGTAGTGAAGTGTCTTATTTGAGCAGTACATCGCTTCTATG 2494
 779 AlaSerSerHisSerThrProGluThrLeuHisCysPheAspThrThrAlaProThrIle 798
 2495 AAATTGCAAGTTTGTCTATGCATCAGGAAGGTTTAAAGAACACAGGACACAGCTCGT 2554
 799 LysLeuAsnLeuThrThrIleArgGlnAspSerPheSerGluLysGlyThrGluGlyArg 818
 2555 GAATTGGAGTAGCGCTTGTGATCTTGTCTTACCTTACCTATCGGATCCGATTTCGATAAG 2614
 819 SerPheAspSerAsnLeuPheAsnLeuSerLeuProIleGlyValLysPheGluLys 838
 2615 GAATCAGACTGCCAAGATGCAACGATCAATCTTCTTGGTTATATCTGTGATCTTGT 2674
 839 PheSerAspCysAsnAspPheSerThrAspLeuThrLeuSerThrValProAspLeuIle 858
 2675 CDTAGTAACCCCGACTGTACGACAACTGCGAATTTAGCGGTGATTTCTTGGAAAACCTTC 2734
 859 ArgAsnAspProLysCysThrThrAlaLeuValIleSerGlyAlaSerTrpGluThrThr 878
 2735 GGTACGAATTTGGCAAGACACTTTAGTCTTCTGTCGAGGAGCAACATTTTTCCTTAAC 2794
 879 AlaAsnAsnLeuAlaArgGlnAlaLeuGlnValArgAlaGlySerHisThrAlaPheSer 898
 2795 TCAAAATTTTGAAGCTTTAGCCAAATTTCTTTTGAATTCGCTGGGTCA 2842
 899 ProMetPheGluValLeuGlyGlnPheValPheGluValArgGlySer 914
 RESULT 11
 AAY90238

ID AAY90238 standard; Protein; 885 AA.
 XX
 AC AAY90238;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Mature Chlamydia antigen CPN100635.
 XX
 KW Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
 KW therapy; upper respiratory tract disease; bronchitis; sinusitis;
 KW asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.
 XX
 OS Chlamydia pneumoniae.
 XX
 PN W0200032794-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 01-DEC-1999; 99WO-CR01147.
 XX
 PR 01-DEC-1998; 98US-0110339.
 PR 01-DEC-1998; 98US-0110340.
 PR 01-DEC-1998; 98US-0110427.
 PR 01-DEC-1998; 98US-0110428.
 PR 01-DEC-1998; 98US-0110438.
 XX
 PA (CONN-) CONNAUGHT LAB LTD.
 XX
 PI Murdin AD, Oomen RP, Wang J;
 XX
 DR WPI: 2000-412339/35.
 DR N-PSDB; AAA30849, AAA30850.
 XX

PT Nucleic acids encoding polypeptide antigens from Chlamydia useful for
 PT preventing, diagnosing and treating diseases such as community acquired
 PT pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
 PT asthma -
 XX
 PS Claim 16; Fig 3; 174pp; English.
 XX
 CC This sequence is a Chlamydia antigen of the inventory, designated
 CC CPN100635. The nucleic acids (and their complementary sequences) may be
 CC used as diagnostic agents for detecting the presence of nucleic acids
 CC encoding Chlamydia antigens in samples according to standard methods,
 CC and therefore, for diagnosing Chlamydia infections. For example, they may
 CC be used as primers and probes for diagnostic polymerase chain reaction
 CC (PCR) assays. Antisense sequences may be used to down regulate
 CC expression of the proteins and may be used to treat infections. The
 CC nucleic acids may also be used to produce the protein antigens they
 CC encode according to standard recombinant DNA methodologies. The
 CC proteins may then be used as antigens for the production of antibodies
 CC (i.e. as vaccines) for preventing infection by Chlamydia. The
 CC antibodies may also be used as diagnostic reagents for detecting
 CC infections. Chlamydia is a pathogen implicated in the development of
 CC (for example) community acquired pneumonia, upper respiratory tract
 CC disease (especially bronchitis and sinusitis, asthmatic bronchitis,
 CC adult-onset asthma and acute exacerbations of asthma in adults.
 XX
 SQ Sequence 885 AA;

Alignment Scores:
 Pred. No.: 7,81e-155 Length: 885
 Score: 1987.50 Matches: 420
 Percent Similarity: 62.12% Conservative: 136
 Best Local Similarity: 46.93% Mismatches: 302
 Query Match: 36.74% Indels: 37
 DB: 21 Gaps: 16

US-09-428-122-1 (1-3000) x AAY90238 (1-885)
 QY 251 GGAAGTACCTACCTATTAAAGGGAATGCTACTCTAGAAATATATCTCTGGAAACAGGCACA 310
 DB 11 GlyleAspTyrLeuThrGlyAspIleThrLeuGlnAsnLeu---GlyAspSerAla 29

QY 311 GCAATCACAAGAGCTGTTTAAACACACTAAGGGCGATTGACTTTCACAGGTAACGGG 370
 DB 30 AlaLeuThrLysGlyCysPheSerAspThrThrGluSerLeuSerPheAlaGlyLysGly 49
 QY 371 AACTCTCTATTGTTCCAAAGCGGTGATCGAGGACTGTAGCAGGGCGTCTGTTAAACAGC 430
 DB 50 TyrSerLeuSerPheLeuAsnIleLysSer---SerAlaGluGlyAlaAlaLeu---Ser 67
 QY 431 AGCGTGGTAGATAAATCTACCGATTATAGGGTTTTCTTCGCTATCTTTATTGCGTCT 490
 DB 68 ValThrThrAspLysAsnLeuSerLeuThrGlyPheSerSerLeuThrPheLeuAlaAla 87
 QY 491 CTTGGAGTTCGATAACTACC-----GGCAAGGAGCGGTAGCTGCTCTACGGGTAGC 544
 DB 88 ProSerSerValIleThrThrProSerGlyLysGlyAlaValLysCysGly---GlyAsp 106
 QY 545 TTGAGTTTGCACAAAATGTCAGTTTCTCAGCAAAACCTTTCAACGGGATAATGGC 604
 DB 107 LeuThrPheAspAsnAsnGlyThrIleLeuPheLysGlnAspTyrCysGluGluAsnGly 126
 QY 605 GGTGCTATCACCGCAAAACTCTTTTCAATTAACAGGAGCTACAAATGTCAGCTCTGTTTTCT 664
 DB 127 GlyAlaIleSerThrLysAsnLeuSerLeuLysAsnSerThrGlySerIleSerPheGlu 146
 QY 665 GAAATACCTCTCA-----AAGNAGGCGGAGCCATTCAGACTCCGATGCCCTT 715
 DB 147 GlyAsnLysSerSerAlaThrGlyLysGlyLysGlyAlaIleCysAlaThrGlyThrVal 166
 QY 716 ACCATTACTGGAACCAAGGGGAAGTCTCTTTTCTGACAAATACTCTTCGGATTCTGGA 775
 DB 167 AspIleThrAsnAsnThrAlaProThrLeuPheSerAsnAsnIleAlaGluAlaGly 186
 QY 776 GCTGCAATTTTACAGAGCGCTCGGTGACTATTCTTAATAATGCTAAAGTTTCTTTATT 835
 DB 187 GlyAlaIleAsnSerThrGlyAsnCysThrIleThrGlyAsnThrSerLeuValPheSer 206
 QY 836 GACAATAAGGTACAGGAGCGAGCTCTCTCAACCGGGGATATGTCAGAGAGTGCTATC 895
 DB 207 GluAsnSerValThr-----AlaThrAlaGly-----AsnGlyGlyAlaLeu 220
 QY 896 TGTGCTTATAAACTAGTACAGATACTAAGTTCACCTCACTGAAATCAGATGTTACTC 955
 DB 221 -----SerGlyAspAlaAspValThrIleSerGlyAsnGlnSerValThr 235
 QY 956 TTCAGCAACAATACATCGACACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTG 1015
 DB 236 PheSerGlyAsnGlnAlaValAlaAsnGlyGlyAlaIleTyrAlaLysLysLeuThrLeu 255
 QY 1016 GCTTCC-----GGAGGACTTACCCTATTTCAGTAGAATAGTGTCAATGGAGGTACGCT 1069
 DB 256 AlaSerGlyGlyGlyGlyAsnProPheSerAsnAsnIleValGlnGlyThrThrAla 275
 QY 1070 CCTAAAGTGGAGCCATAGCTATCGAAGATAGTGGGAATTTGAGTTTATCCGCGGATAGT 1129
 DB 276 GlyAsnGlyGlyAlaIleSerIleLeuAlaAlaGlyGluCysSerLeuPheSerGluAla 295
 QY 1130 GGTGCACATTGCTTTTTTAGGGAATACAGTCACTTCTACTACTCT---GGGACGAATAGA 1186
 DB 296 GlyAspHisTyrLeuAsnGlyAsnAlaIleValAlaThrThrProGlnThrThrLysArg 315
 QY 1187 AGTAGTATCGACTTAGAACGAGTGCACAGATCAGAGCTTTGCTGCTGCTGCTGCTGCTG 1246
 DB 316 AsnSerIleAspIleGlySerThrGlyLysAspHisGluLeuArgAlaIleSerGlyHis 335
 QY 1247 GCCATCTACTTCTATGATCCATAACTACAGGATCATCCACAGTATCAGAGTGTCTTA 1306
 DB 336 SerIlePhePheTyrAspProIleThrAlaAsnThrAlaAlaAspSerThrAspThrLeu 355
 QY 1307 AAGATTAAATGAGACTCCGGCAGATTCTGCACTCAATATATACAGGGAACATCATCTTCA 1366
 DB 356 AsnLeuAsnLysAlaAlaAlaGlyAsnSerThrAspTyrSerGlySerIleValPheSer 375

QY 1367 GGAGAAAGTTATCAGACAGAGCCGACGATCTCTAAATCTTACTTCCAGACTACTA 1426
DB 376 GlyGluLysLeuSerGluAspGluAlaLysValAlaAspAsnLeuThrSerThrLeuLys 395
QY 1427 CAGCTGTAACTCTTCAGGAGGTACTTCTTAAACATGAGTGACCTCAGACT 1486
DB 396 GlnProValThrLeuThrAlaGlyAsnLeuValLeuLysArgGlyValThrLeuAspThr 415
QY 1487 CAGGCATTCACTCAACAGCCAGATTCTCGTCTCGAAATGGAGTAGGAACTACTAGAA 1546
DB 416 LysGlyPheThrGlnThrAlaGlySerSerValIleMetAspAlaGlyThrThrLeuLys 435
QY 1547 CTTCTCT--GATPACTAGCACCATAACAATTGGTCATTATCATCATCAGTCTTATAGACCGT 1603
DB 436 AlaSerThrGluGluValThrLeuThrGlyLeuSerIleProValAspSerLeuGlyGlu 455
QY 1604 GCAAAGAGGCAAAATAGAACCAAGCTAGTCAAAAAATCTCACTTTATCTGGAACC 1663
DB 456 GlyLysLysValValIleAlaAlaSerAlaAlaSerLysAsnValAlaLeuSerGlyPro 475
QY 1664 ATCACTTTATTGGACCCGACGGCCAGCTTTTATGAAATCATAGTTTAAAGAAATCCTCAG 1723
DB 476 IleLeuLeuLeuAspAsnGlnGlyAsnAlaTyrGluAsnHisAspLeuGlyLysThrGln 495
QY 1724 TCCTAGCATCTTACAGCTCAAGCTTCTGGAACCTGTAACAGACCCGACGACTCCA 1783
DB 496 AspPheSerPheValGlnLeuSerAlaLeuGlyThrAlaThrThrAspValProAla 515
QY 1784 GATCTCTAATGGTGAGAAATCCATTACGGCTATCAGGGAACCTGGGGCCCAATGTT 1843
DB 516 ValProThrValAlaThrProThrHisTyrGlyTyrGlnGlyThrTyrGly--MetThr 534
QY 1844 TGG-----GGGACAGGGGCTTCTACGACTGCAACCTCACTGCACTAA 1888
DB 535 TrpValAspAspThrAlaSerThrProLysThrLysThrAlaThrLeuAlaTrpThrAsn 554
QY 1889 ACTGGCTATATCTTCAATCCGAGCTATCGCTCTTATGCTCCCTAATAGCTTATGGAT 1948
DB 555 ThrGlyTyrLeuProAsnProGluArgGlnGlyProLeuValProAsnSerLeuTrpGly 574
QY 1949 GCATTTATAGATATAGCTCTCTCCATTATTCGAGACTGCAACGAAAGGGTTGACAG 2008
DB 575 SerPheSerAspIleGlnIleGlnGlyValIleGluArgSerAlaLeuThrLeuCys 594
QY 2009 CGAGACCGCTCTTTTGGTGTGCTGATTATCTPACTTCTTCATAGGATAGTACAAA 2068
DB 595 SerAspArgGlyPheTrpAlaAlaGlyValAlaAsnPheLeuAspLysAspLysGly 614
QY 2069 ACAGACGGGGTTTCGCCATTTGAGTGGGGTTATGTCATAGAGGAAACCTACATAT 2128
DB 615 GluLysArgLysTyrArgHisLysSerGlyGlyTyrAlaIleGlyGlyAlaAlaGlnThr 634
QY 2129 TGTTCAGATAAGATTCTTAGTGTGCTTGTGCTCTTTGAGAGATAGAGACTAC 2188
DB 635 CysSerGluAsnLeuIleSerPheAlaPheCysGlnLeuPheGlySerAspLysAspPhe 654
QY 2189 TTTGTAGCTAAGATCAAGTACAGTCTCAGGAGAACTCTCTTATACGACGACACGAA 2248
DB 655 LeuValAlaLysAsnHisThrAspThrThrAlaGlyAlaPheTyrIleGlnHis----- 672
QY 2249 ACCTATATCTCTCTTCCTCAAACTACGGCTTGTTCGTTGCTTATGTTCTCT----- 2302
DB 673 -----IleThrGluCysSerGlyPheIleGlyCysLeuLeuAspLysLeuProGlySer 690
QY 2303 ---ACAGAGATTCCTGTCTCTTTTCAGGAAACCTTAGCTACACCCATAGGTAACGAT 2359
DB 691 TrpSerHisLysProLeuValLeuGluGlyGlnLeuAlaTyrSerHisValSerAsnAsp 710
QY 2360 CTGAAAACCAAGTATACAAATATCTCTAGTCTTAAAGAAAGCTGGGGGAATGATGTTTC 2419
DB 711 LeuLysThrLysTyrThrAlaTyrProGluValLysGlySerTrpGlyAsnAlaPhe 730
QY 2420 GCTTTAGAAATCGGTGGAGAGCTCCGATTGCTTAGTAGAAAGTGTCTTATTGACGAG 2479

DB 731 AsnMetMetLeuGlyAlaSerSerHisSerTyrProGluTyrLeuHisCysPheAspThr 750
QY 2480 TACATGCCCTTCATGAATTCGAGTTTGTCTATGCATCATCAGGAAGGTTTTAAAGAACAG 2539
DB 751 TyrAlaProTyrIleLysLeuAsnLeuThrTyrIleArgGlnAspSerPheSerGluLys 770
QY 2540 GGRACAGAACTCGTGAATTTGGAGTAGCCGCTTGTGTAATCTTGCTTACCTATCGGG 2599
DB 771 GlyThrGluGlyArgSerPheAspSerAsnLeuPheAsnLeuSerLeuProIleGly 790
QY 2600 ATCCGATTTCATAGGAATCAGACTGCAAGATGCAACGTAACATCTAATCTTTGGTTAT 2659
DB 791 ValLysPheGluLysPheSerAspCysAsnAspPheSerTyrAspLeuThrLeuSerTyr 810
QY 2660 ACTGTGATCTTGTCTGTAGTAACCCGACGCTGACGACACACTGCGAANTAGCGGTGAT 2719
DB 811 ValProAspLeuIleArgAsnAspProLysCysThrThrAlaLeuValIleSerGlyAla 830
QY 2720 TCTTGGAAACCTTCGGTACGATTTGCAAGTTCGCAAGCAAGCTTTAGCTTCGTCAGGGAAC 2779
DB 831 SerTrpGluThrThrAlaAsnAsnLeuAlaArgGlnAlaLeuGlnValArgAlaGlySer 850
QY 2780 CATTTTGTCTTAACTCAAAATTTTGAAGCCCTTTAGCCCAATTTCTTTGAATTCGCTGG 2839
DB 851 HistyralaPheSerProMetPheGluValLeuGlyGlnPheValPheGluValArgGly 870
QY 2840 TCATCTCGCAATTCATAGTGTAGCTTAGGACCAAAATACCAATTC 2884
DB 871 SerSerArgIleTyrAsnValAspLeuGlyGlyLysPheGlnPhe 885
RESULT 12
AAW88423 standard; Protein; 928 AA.
ID AAW88423
XX AC AAW88423;
XX DT 26-APR-1999 (first entry)
XX DE Chlamydia pneumoniae surface exposed protein Omp10.
XX KW Omp10; outer membrane protein 10; surface exposed protein;
XX KW antigen; infection; diagnosis; vaccine; atherosclerosis; asthma.
XX OS Chlamydia pneumoniae.
XX PN WO9858953-A2.
XX PD 30-DEC-1998.
XX PF 19-JUN-1998; 98WO-DK00266.
XX PR 23-JUN-1997; 97DK-0000744.
XX PA (BIRK/) BIRKELUND S.
XX PA (CHRI/) CHRISTIANSEN G.
XX XX Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Mygind P;
XX DR WPI; 1999-105610/09.
XX DR N-PSDB; AAW06822.
XX PT Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT these proteins
XX PS Claim 7; Page 60-62; 115pp; English.
XX CC This polypeptide comprises the novel 98.4 kDa surface exposed
CC protein Omp10 of the human respiratory pathogen Chlamydia
CC pneumoniae. Its amino acid sequence was deduced from DNA (see

CC AAX06822) isolated from a C. pneumoniae expression library. The
 CC invention provides 12 novel surface exposed proteins, Omp4-Omp15
 CC (see AAW88417-28), and nucleic acid sequences encoding them (see
 CC AAX06816-27). A new species specific test is claimed that is used
 CC to identify mammals (including humans) infected with Chlamydia
 CC pneumoniae. The test comprises detecting antibodies specific for
 CC Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
 CC membrane proteins, especially by PCR. The proteins are also used
 CC in the diagnosis of C. pneumoniae infection in mammals. The
 CC nucleic acids and proteins can also be used in the immunization of
 CC mammals, the nucleic acids being particularly useful as DNA
 CC vaccines for effecting in vivo expression of antigens. The
 CC vaccines may also prevent atherosclerosis and bronchial asthma,
 CC which are possibly associated with C. pneumoniae.

XX Sequence 928 AA;

Alignment Scores:
 Pred. No.: 1,06e-154 Length: 928
 Score: 1986.00 Matches: 430
 Percent Similarity: 60.95% Conservative: 149
 Best Local Similarity: 45.26% Mismatches: 327
 Query Match: 36.72% Indels: 44
 DB: 20 Gaps: 19

US-09-428-122-1 (1-3000) x AAW88423 (1-928)

Qy 101 ATGAAGTCTCTTCCCAAGTTGTATTTCTACATTTGCTATTTCCCTTGTCTATG 160
 Db 1 MetLysSerSerLeuHisTsrPheValIleSerSerLeuAlaLeuProLeuSerLeu 20
 Qy 161 -----ATTGTCACCGAGACAGTTTGGATTCAAGTCGCGATTCGAT 202
 Db 21 AsnPheSerAlaPheAlaAlaValIleGluLeuAsnLeuGlyProThrAsnSerPheSer 40
 Qy 203 GGGAAATAAATGGTAATTTTCAGTTCGTGAGATCAGGAAGATGCT---GGAACTACC 259
 Db 41 Gly-----ProGlyThyTrpThrProAlaGlnThrThrAsnAlaAspGlyThrIle 58
 Qy 260 TACCTATTAAAGGAATGTCACTCTAGAAATATTCCTGGAACAGGCACGCAATCACA 319
 Db 59 TyrAsnLeuThrGlyAspValSerIleThrAsn---AlaGlySerProThrAlaLeuThr 77
 Qy 320 AAAAGCTTTTAAACACACATAAGGCGATTGTACTTTCACAGGTAAAGGCACTCTCTA 379
 Db 78 AlaSerCysPheLysGluThrThrGlyAsnLeuSerPheGlnGlyHisGlyTyrGlnPhe 97
 Qy 380 TTGTTCCAAACGGTGGATGACAGGACTAGCAGGGGCTGCTGTTTAAACAGCAGCGTGTA 439
 Db 98 LeuLeuGlnAsnIleAspAlaGly-----AlaAsnCysThrPheThrAsnThrAlaAla 115
 Qy 440 GATAAATCTACACGTTTATAGGGTTTCTTCGCTATCTTTATGCGTCTCTCTGGAAGT 499
 Db 116 AsnLysLeuSerPheSerGlyPheSerGlyLeuSerLeuIleGlnThr-----Thr 133
 Qy 500 TCGATACTACGGCAAGAGCCGTTAGCTCTACGGGTAGCTTGCAGTTTGACAAA 559
 Db 134 AsnAlaThrThrGlyThrGlyAlaIleLys---SerThrGlyAlaCysSerIleGlnSer 152
 Qy 560 AATGTCAGTTTCTCTCAGCAAAAACCTTTCAACGGGATAATGGGGTCTATCACCGCA 619
 Db 153 AsnTyrSerCysTyrPheLysGlnAsnPheSerAsnAspAsnGlyAlaLeuGlnGly 172
 Qy 620 AAAAATCTTTTCAACAGGCACTCAATGTCTGAGCTCTGTTTCTGAAAATACCTCTCA 679
 Db 173 SerSerIleSerLeuSer---LeuAsnProAsnLeuThrPheAlaLysAsnLysAlaThr 191
 Qy 680 AAGAAAGCGGAGCCATTCAGATCTTCGATGCCCTTACATCTACTGGAACCAAGGGGAA 739
 Db 192 GlnLysGlyGlyAlaLeuTyrSerThrGlyGlyIleThrIleAsnAsnThrLeuAsnSer 211
 Qy 740 GTCCTCTTTTCTGCAATCTCTCTCGGATTCGAGCTGCAATTTTACAGAGCCCTCG 799

Db 212 AlaSerPheSerGluAsnThrAlaAlaAsnAsnGlyGlyAlaIleTyrThrGluAlaSer 231
 Qy 800 GTGACTATTCTTAATGCTAAAGTTCTTTTATTTCACAAATAGGTCAAGGCGAGC 859
 Db 232 SerPheIleSerSerAsnLysAlaIleSerPheIleAsnAsnSerValThrAlaThrSer 251
 Qy 860 TCCTCAACACACGGGGATATGTCAGGAGTGCTATCTGTCTTATAAACTAGTACAGAT 919
 Db 252 Ala-----ThrGlyGlyAlaIleTyrCysSerSerThrSerAlaPro 265
 Qy 920 ACTAAGGTC---ACCCTCACTGGAATACAGATTTACTTCTTACGCAACAATACATCGACA 976
 Db 266 LysProValLeuThrLeuSerAspAsnGlyGluLeuAsnPheIleGlyAsnThrAlaIle 285
 Qy 977 ACAGCGGAGGAGCTATCTATGTGAAAAGCTGAACTGCTCGGAGGAGCTTACCCCTA 1036
 Db 286 ThrSerGlyGlyAlaIleTyrThrAspAsnLeuValLeuSerSerGlyGlyProThrLeu 305
 Qy 1037 TTCAGTAGAATAAGTGTCAATGGAGGTACAGCTCTTAAAGCTGAGCATAGTATCGAA 1096
 Db 306 PheLysAsnAsnSerAlaIleAspThrAlaAlaProLeuGlyGlyAlaIleAlaIleAla 325
 Qy 1097 GATAGTGGGGAATTGAGTTTATCCGCGATAGTGGTGACATTGCTTTTTAGGGAATACA 1156
 Db 326 AspSerGlySerLeuSerLeuSerAlaLeuGlyGlyAspIleThrPheGluGlyAsnThr 345
 Qy 1157 GTC-----ACTTCTACTCTCTGGGAGCAATAGAGTAGTAGTATCGACTTAGGA--- 1204
 Db 346 ValValLysGlyAlaSerSerGlnThrThrArgAsnSerIleAsnIleGlyAsn 365
 Qy 1205 ACAGTCCAAAGATGACAGCTTTGCTGCTGCTGAGCCATCTACTTCTATGAT 1264
 Db 366 ThrAsnAlaIleValGlnLeuAlaGlnAsnGlnGlyAsnThrIleTyrPheTyrAsp 385
 Qy 1265 CCCATACTACAGGATCATCCACACAGTTTACAGATGCTCTTAAAGTTAATAGACTCCG 1324
 Db 386 ProIleThrThrAsnHisThrAlaAlaLeuSerAspAlaLeuAsnLeuAsnGlyProAsp 405
 Qy 1325 GCAGATTCTGCACATAATATACAGGAAATCATCTTTCACAGGAAAAGTTATCAGAG 1384
 Db 406 LeuAlaGlyAsnProAlaTyrGlnGlyThrIleValPheSerGlyGlyLysLeuSerGlu 425
 Qy 1385 ACAGAGCCCGACAGTCTTAAATCTTCTTCAAGCTACTACAGCTGTAACTCTTCA 1444
 Db 426 AlaGluAlaAlaGluAlaAspAsnLeuLysSerThrIleGlnGlnProLeuThrLeuAla 445
 Qy 1445 GGAGTACTCTATCTTTAAACATGAGTGACTCTGCAGACTCAGGATTCACCTCAACAG 1504
 Db 446 GlyGlyGlnLeuSerLeuLysSerGlyValThrLeuValAlaLysSerPheSerGlnSer 465
 Qy 1505 GCAGATTCTGCTCGAATGGAGCTAGGAACTACTCTAGAACCTGCTGATAGTACACC 1564
 Db 466 ProGlySerThrLeuLeuMetAspAlaGlyThrThrLeuGluThrAlaAspGlyIleThr 485
 Qy 1565 ATAAACAAATTTGGTCATTAAACATCAGTTCTATAGACGTGCAAGAGGCAAAATAGAA 1624
 Db 486 IleAsnAsnLeuValLeuAsnValAspSerLeuLysGlnThrLysAlaThrLeuLys 505
 Qy 1625 ACCAAAGCTACGTCAAAAATCTGACTTTTATCTGGAACCATCACTTATTGAGCCGACG 1684
 Db 506 AlaThrGlnAlaSerGlnThrValThrLeuSerGlySerLeuSerLeuValAspProSer 525
 Qy 1685 GGCAGTTTATGAAATCATAGTTTAAAGAAATCTCAGTCTCCTACGACATCTTAGAGTCT 1744
 Db 526 GlyAsnValTyrGluAspValSerTrpAsnAsnProGlnValPheSerCysLeuThrLeu 545
 Qy 1745 AAAGCTCTCT---GGAACTGTAAACAGCAGCCAGTCTCCAGATCTCTATATATGGT 1798
 Db 546 ThrAlaAspAspProAlaAsnIleHisIleThrAspLeuAlaAlaAspProLeuGluLys 565
 Qy 1799 GAGAAATTTCCATTACCGGCTATCAGGAACTTTGGGGCCCAATTTGTTGGGACACGGGCT 1858
 Db 566 AsnProIleHisTsrPglyTyrGlnGlyAsnTrpAla---LeuSerTrpGlnGluAspThr 584

| | | | |
|----|------|--|------|
| QY | 1859 | TCTACG-----ACTGCAACCTTCAACTGGACTAAACCTGGCTATATATCTTAATCCC | 1909 |
| Db | 585 | AlaThrLysSerLysAlaAlaThrLeuThrTrpThrLysThrGlyTyrAsnProAsnPro | 604 |
| QY | 1910 | GAGCGTATCGGCTCTTTAGTCCTTAATAGCTTATGGAATGCAATTTATAGATATAGCTCT | 1969 |
| Db | 605 | GluArgArgGlyThrLeuValAlaAsnThrLeuTrpGlySerPheValAspValArgSer | 624 |
| QY | 1970 | CTCCATTATCTTATCGAGACTCAAAACGAAGGTTGCGAGGAGACCGTGCTTTTGGTGT | 2029 |
| Db | 625 | IleGlnGlnLeuValAlaThrLysValArgGlnSerGlnGluThrArgGlyIleTrpCys | 644 |
| QY | 2030 | GCTGGATTATCACTCTTCCATAAGGATAGTACAAAACACGACGGGGTTTCGCAT | 2089 |
| Db | 645 | GluGlyIleSerAsnPhePheHisLysAspSerThrLysIleAsnLysGlyPheArgHis | 664 |
| QY | 2090 | TTGAGTGGCGGTTATGTCTAGAGGAACCTACATCTTGTTCAGATAAGATTCTTAGT | 2149 |
| Db | 665 | IleSerAlaGlyTyrValValGlyAlaThrThrLeuAlaSerAspAsnLeuIleThr | 684 |
| QY | 2150 | GCTGCATTTTGTCACTCTTGAAGAGATAGAGACTACTTTGTAGCTAAGAAATCAAGT | 2209 |
| Db | 685 | AlaAlaPheCysGlnLeuPheGlyLysAspArgAspHisPheIleAsnLysAsnArgAla | 704 |
| QY | 2210 | ACAGTCTACGAGGAACTCTCTATTACACGACAAACCTATATCTCTCTCTCTCTGC | 2269 |
| Db | 705 | SerAlaTyrAlaAlaSerLeuHisLeuGlnHisLeuAlaThrLeuSerSer | 721 |
| QY | 2270 | AACTAGGCGCTTGTTCGTGTCTTATGTCCT-----ACAGAGATTCTGTCTC | 2320 |
| Db | 722 | -----ProSerLeuLeuArgTyrLeuProGlySerGluSerGlnProValLeu | 738 |
| QY | 2321 | TTTTTCAGGAAACCTTACCTACCCATACGATACGATCTGAAACCAAGTATATCAACA | 2380 |
| Db | 739 | PheAspAlaGlnIleSerTyrIleTyrSerLysAsnThrMetLysThrTyrTyrThrGln | 758 |
| QY | 2381 | TAPCTACTGTTAAAGAAAGCTGGGGAATGATAGTTTCGTTTAGAATTCGGTGGAAAG | 2440 |
| Db | 759 | AlaProLysGlyGluSerSerTyrTyrAsnAspGlyCysAlaLeuGluLeuAlaSerSer | 778 |
| QY | 2441 | GCTCCG---ATTGCTTAGTAAAGTGCTCTATTGAGCAGTACATGCCCTTCATGAA | 2497 |
| Db | 779 | LeuProHisThrAlaLeuSerHisGluGlyLeuPheHisAlaTyrPheProPheIleLys | 798 |
| QY | 2498 | TTGCGATTGCTCTATGCATCAGGAAGGTTTAAAGAACAGGAAACAGAA---GCTCGT | 2554 |
| Db | 799 | ValGluAlaSerTyrIleHisGlnAspSerPheLysGluArgAsnThrThrLeuValArg | 818 |
| QY | 2555 | GAATTGGAAAGTACCGCTCTTGTAATCTTGCCCTTACCTATCGGATCCGATTTGATAAG | 2614 |
| Db | 819 | SerPheAspSerGlyAspLeuIleAsnValSerValProIleGlyIleThrPheGluArg | 838 |
| QY | 2615 | GAATCAGACTGCCAAGATCAACGTACAATCTCTGTTTACTCTGTTGATCTTGT | 2674 |
| Db | 839 | PheSerArgAsnGluArgAlaSerTyrGluAlaThrValIleTyrValAlaAspValTyr | 858 |
| QY | 2675 | CGTAGTAACCCCGACTGTACGACAACACTGCGAATTAGCGGTGATCTTCGAAACCTTC | 2734 |
| Db | 859 | ArgLysAsnProAspCysThrThrAlaLeuLeuIleAsnAsnThrSerTyrLysThrThr | 878 |
| QY | 2735 | GGTACGAATTTGGCAAGACGCTTTAGTCTTCCTGTCGAGGAACCAATTTTCTTAAC | 2794 |
| Db | 879 | GlyThrAsnLeuSerArgGlnAlaGlyIleGlyArgAlaGlyIlePheTyrAlaPheSer | 898 |
| QY | 2795 | TCAATTTGAGCTTTAGCAATTTCTTTCAATTGGTGGTGTCTATCTCGCAATTAC | 2854 |
| Db | 899 | ProAsnLeuGluValThrSerAsnLeuSerMetCysIleArgGlySerArgSerTyr | 918 |
| QY | 2855 | AATGTAGACTTAGGAGCAAAATACCAATTC | 2884 |
| Db | 919 | AsnAlaAspLeuGlyGlyLysPheGlnPhe | 928 |

RESULT 13
ABB90542 standard; Protein; 928 AA.
XX ABB90542;
XX 29-JUL-2002 (first entry)
XX Chlamydia pneumoniae cp6731 protein, SEQ ID NO:33.
XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW human respiratory disease; cardiovascular disease; atherosclerosis;
KW coronary artery disease; carotid artery stenosis; myocardial infarction;
KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW strain CWL029.
XX Chlamydia pneumoniae.
XX Key Location/Qualifiers
FT Peptide 1..26
FT Protein /label= Signal_peptide 27..928
FT /note= "Mature protein"
XX WO200202606-A2.
XX 10-JAN-2002.
XX 03-JUL-2001; 2001WO-IB01445.
XX 03-JUL-2000; 2000GB-0016363.
PR 11-JUL-2000; 2000GB-0017047.
PR 21-JUL-2000; 2000GB-0017983.
PR 07-AUG-2000; 2000GB-0019368.
PR 18-AUG-2000; 2000GB-0020440.
PR 14-SEP-2000; 2000GB-0022583.
PR 10-NOV-2000; 2000GB-0027549.
PR 22-DEC-2000; 2000GB-0031706.
XX (CHIR-) CHIRON SPA.
XX Ratti G, Grandi G;
XX WPI; 2002-154726/20.
DR N-PSDB; ABL91200.
XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes -
XX Claim 1; Page 57; 364pp; English.
XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC them. The proteins are predicted to be immunogenic and may therefore be
CC useful in vaccine production and for diagnostic purposes. Chlamydia
CC pneumoniae is a common cause of respiratory disease in humans, and is
CC also involved in the development of cardiovascular diseases such as
CC atherosclerosis, coronary artery disease, carotid artery stenosis,
CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC claudication and stroke. The proteins and nucleic acids of the invention
CC may be used in vaccines and pharmaceutical compositions for the
CC prevention or treatment of chlamydial infections, particularly Chlamydia
CC pneumoniae infections. The proteins may also be used in the detection of
CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC DNA probe assay or blotting techniques for determining Chlamydia
CC pneumoniae gene expression. The present sequence represents a
CC specifically claimed Chlamydia pneumoniae protein of the invention.
SQ Sequence 928 AA;
Alignment Scores: 2.25e-154 Length: 928
Pred. No.:

Score: 1982.00 Matches: 429
Percent Similarity: 60.95% Conservative: 150
Best Local Similarity: 45.16% Mismatches: 327
Query Match: 36.64% Indels: 44
DB: 23 Gaps: 19

us-09-428-122-1 (1-3000) x ABB90542 (1-928)

```
QY 101 ATGAAGCTCTTCCCAAGTTGTATTTCTACATTTGCTATTTCCCTTCTCTATG 160
DB 1 MetlySerLeuHisTTPheLeuSerLeuAlaLeuProLeuSerLeu 20
QY 161 -----ATTGCTACCGACGACAGTTTGGATTCAAGTCGAGTTTCGAT 202
DB 21 AsnPheSerAlaPheAlaValGluLeuLeuGlyProThrAsnSerPheSer 40
QY 203 GGGAAATAAATGGTAAATTTTCAGTTCGTGAGAGTCAGGAAGATGCT---GGAACTACC 259
DB 41 Gly-----ProGlyThrTyThrProProAlaGlnThrThrAsnAlaAspGlyThrIle 58
QY 260 TACCTATTTAAGGAAATGTCATCTAGAAATATTCCTGGAACAGGCACGACATCA 319
DB 59 TyrAsnLeuThrGlyAspValSerIleThrAsn---AlaGlySerProThrAlaLeuThr 77
QY 320 AAAAGCTGTTTAAACACACTAAGGGCGATTGTACTTTTCACAGGTAAACGGAACTCTCTA 379
DB 78 AlaSerCysPheLeuGluThrThrGlyAsnLeuSerPheGlnGlyHisGlyTyGlnPhe 97
QY 380 TTGTTCCAAACGGTGGATGTCAGGGGACTGTAGCAGGGGCTGCTGTTTAAACAGCAGCGTGTGA 439
DB 98 LeuLeuGlnAsnIleAspAlaGly-----AlaAsnCysThrPheThrAsnThrAlaAla 115
QY 440 GATAAATCTACACAGTTTATAGGGTTTCTCGCTATCTTTATGCTCTCTCTGGAAGT 499
DB 116 AsnIleLeuLeuSerPheSerGlyPheSerTyLeuSerLeuIleGlnThr-----Thr 133
QY 500 TCGATAACTACCGGCAAGGAGCCGTAGTCTCTACGGGTAGCTTGGATTGACAAA 559
DB 134 AsnAlaThrThrGlyThrGlyAlaIleIlys---SerThrGlyAlaCysSerIleGlnSer 152
QY 560 AATGTCAGTTTCTCTCAGCAAAACATTTCAACGGGTAATGCGGTGCTATCACCCCA 619
DB 153 AsnTySerCysTyThrPheGlyGlnAsnPheSerAsnAspAsnGlyGlyAlaLeuGlnGly 172
QY 620 AAAACTCTTTCAACAGGACTACATGTCAGCTCTGTTTCTGAAATACCTCTCA 679
DB 173 SerSerIleSerLeuSer---LeuAsnProAsnLeuThrPheAlaIleAsnLysAlaThr 191
QY 680 AAGAAAGCGGAGCATTACAGACTTCGATGCCCTTACCATCTACTGGAACCAAGGGAA 739
DB 192 GlnIysGlyGlyAlaLeuTySerThrGlyGlyIleThrIleAsnAsnThrLeuAsnSer 211
QY 740 GTCCTCTTTTCTGCAATCTCTCTGGAATCTGGAATCTGGAATCTGCAATTTTACAGACCTCG 799
DB 212 AlaSerPheSerGluAsnThrAlaAlaAsnAsnGlyGlyAlaIleTyThrGluAlaSer 231
QY 800 GTGACTATTTCTAATGCTAAAGTCTTCTTATGACATAAGCTCACAGGCGGAGC 859
DB 232 SerPheIleSerAsnLysAlaIleSerPheIleAsnAsnSerValThrAlaThrSer 251
QY 860 TCCTCAACAAACGGGGATATGTCAGAGGTGCTATCTGTGCTTATAAACTAGTACAGAT 919
DB 252 Ala-----ThrGlyGlyAlaIleTyCysSerSerThrSerAlaPro 265
QY 920 ACTAAGGTC---ACCTCAGCTGGAATCAGATGTTTACTCTCTCAGCAACAATACATCGACA 976
DB 266 LysProValLeuThrLeuSerAspAsnGlyGluLeuAsnPheIleGlyAsnThrAlaIle 285
QY 977 ACAGCGGAGGAGCTATCTATCTGAAAAGCTCGAATCTGGCTTCGGAGGACTTACCCTA 1036
DB 286 ThrSerGlyGlyAlaIleTyThrAspAsnLeuValLeuSerSerGlyGlyProThrLeu 305
QY 1037 TTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTTAAAGGTGGAGCCATAGCTATCGAA 1096
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DB 306 PheIysAsnAsnSerAlaIleAspThrAlaAlaProLeuGlyGlyAlaIleAlaIleAla 325
QY 1097 GATAGTCGGGAATGAGTTTATTCGCGGATAGTGGTGACATGTTCTTTTATAGGAATACA 1156
DB 326 AspSerGlySerLeuSerLeuAlaLeuGlyGlyAspIleThrPheGluGlyAsnThr 345
QY 1157 GTC-----ACTTCTACTCTCTCGGACGAATAAGTAGTAGTATCGACTTAGGA--- 1204
DB 346 ValValIysGlyAlaSerSerGlnThrThrArgAsnSerIleAsnIleGlyAsn 365
QY 1205 ACAGATGCCAAGATGACAGCTTTTCGCTTCTGCTGCTGAGCCATCTACTTCTATCAT 1264
DB 366 ThrAsnAlaIysIleValGlnLeuArgAlaSerGlnGlyAsnThrIleTyPheTyAsp 385
QY 1265 CCCATACTACAGGATCATCCACACAGTTTACAGATGCTCTTAAAGTTTAAAGACTCCG 1324
DB 386 ProIleThrThrSerIleThrAlaAlaLeuSerAspAlaLeuAsnLeuAsnGlyProAsp 405
QY 1325 GCAGATTCTGCACCTACAAATATACAGGGAACATCATCTTTCACAGGAGAAAAGTTATCAGAG 1384
DB 406 LeuAlaGlyAsnProAlaTyGlnGlyThrIleValPheSerGlyGlyLeuSerGlu 425
QY 1385 ACAGAGCCCGCAGATTCTTAAAAATCTTACTTTCGAAGCTACTACAGCCTGTAACCTTTTCA 1444
DB 426 AlaGluAlaAlaGluAlaAspAsnLeuLysSerThrIleGlnGlnProLeuThrLeuAla 445
QY 1445 GGAGTACTCTATCTTTAAACATGAGTGACTCTCGAGACTCAGGACTCAGGACTCAGCAAG 1504
DB 446 GlyGlyGlnLeuSerLeuLysSerGlyValThrLeuValAlaLysSerPheSerGlnSer 465
QY 1505 GCAGATTCTGCTCTCGAAATGAGGAGTAGGAATCTCTAGAACCTGCTGATPACTAGCACC 1564
DB 466 ProGlySerThrLeuLeuMetAspAlaGlyThrThrLeuGluThrAlaAspGlyIleThr 485
QY 1565 ATAAACAATTTGGTCAATTAACATCAGTTTATAGACCGTGCAAAAGAGGCAAAATAGAA 1624
DB 486 IleAsnAsnLeuValLeuAsnValAspSerLeuLysGluThrLysLysAlaThrLeuLys 505
QY 1625 ACCAAAGCTAGCTCAAAATCTGACTTATCTGGAACCATCATCTTATTCGACCGCAGC 1684
DB 506 AlaThrGlnAlaSerGlnThrValThrLeuSerGlySerLeuSerLeuValAspProSer 525
QY 1685 GGCAGCTTTTATGAAATCATAGTTTAAAGAAATCTCAGTCTCAGCATCTTACAGAGCTC 1744
DB 526 GlyAsnValTyGluAspValSerTyPheAsnAsnProGlnValPheSerCysLeuThrLeu 545
QY 1745 AAAGCTTCT-----GGAACGTGTAACAGCACCGCAGTGACTCCAGATCTCTAATGGGT 1798
DB 546 ThrAlaAspAspProAlaAsnIleHisIleThrAspLeuAlaAlaAspProLeuGluLys 565
QY 1799 GAGAAATTCGATTACGCTATCAGGAACTTGGGGCCCAATGTTTGGGGACAGGGGCT 1858
DB 566 AsnProIleHisIleTyGlyTyGlnGlyAsnTrpAla---LeuSerTyGlnGluAspThr 584
QY 1859 TCTACG-----ACTGCAACCTTCAACTGGGAACTGCTATATCTCTAATATCCC 1909
DB 595 AlaThrLysSerLysAlaAlaThrLeuThrTyThrIleThrGlyTyThrAsnProAsnPro 604
QY 1910 GAGCGTATCGCTCTTTAGTCCCTTAATAGCTTATGGAATGCAATTTATAGATATTAGTCT 1969
DB 605 GluArgGlyThrLeuValAlaAsnThrLeuTyGlySerPheValAspValArgSer 624
QY 1970 CTCATATCTTATGAGACTGCAACGAGGCTTGCAGGAGACCGCTGCTTTTGGTGT 2029
DB 625 IleGlnGlnLeuValAlaThrLysValArgGlnSerGlnGluThrArgGlyIleTyTrpCys 644
QY 2030 GCTGATTTATCTTCTTCCATTAAGATAGTACAAAACACGACGCGGCTTCGCCAT 2089
DB 645 GluGlyIleSerAsnPhePheHisLysAspSerThrIleAsnLysGlyPheArgHis 664
QY 2090 TTGAGTGGCGGCTTATGTCATAGGAGGAAACCTACATACTTCTGTCAGATAAGATCTTAGT 2149
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Db 665 IleSerAlaGlyTyrValValGlyAlaThrThrLeuAlaSerAspAsnLeuLeuThr 684
 QY 2150 GCTGATTTTGTACGCTTTTGGAGAGATAGACTACTTTGTAGCTTAAGAATCAAGGT 2209
 Db 685 AlaAlaPheCysGlnLeuPheGlyLysAspArgHisPheIleAsnLysAsnArgAla 704
 QY 2210 ACAGTCTACGAGGAACTCTTATTACAGACACAAACCTATATCTCTTCTTCCTTGC 2269
 Db 705 SerAlaTyrAlaAlaSerLeuHisLeuGlnHisLeuAlaThrLeuSer----- 721
 QY 2270 AAACCTACGGCTTGTCTGTCTTATGTTCT-----ACAGAGATTCTCTTCTC 2320
 Db 722 -----ProSerLeuLeuArgTyrLeuProGlySerGluSerGluGlnProValLeu 738
 QY 2321 TTTTCAGGAACTTAGCTACACCCATACGGATACGATCTGAAACCAAGTATACACA 2380
 Db 739 PheAspAlaGlnIleSerTyrIleTyrSerLysAsnThrMetLysThrTyrThrGln 758
 QY 2381 TATCTACTGTTAAAGGAAGCTGGGGATGATAGTTTCGCTTTAGATTTCGGTGAAGA 2440
 Db 759 AlaProLysGlyGluSerSerTrpTyrAsnAspGlyCysAlaLeuGluLeuAlaSerSer 778
 QY 2441 GCTCCG---ATTGCTCTAGATGAAGTCTCTATTGACGATCATGCGCTTCATGAA 2497
 Db 779 LeuProHisThrAlaLeuSerHisGluGlyLeuPheHisAlaTyrPheProPheIleLys 798
 QY 2498 TTGCAAGTTTGTCTATGCATACAGAGGTTTAAAGAACAGGGAACAGAA---GCTCGT 2554
 Db 799 ValGluAlaSerTyrIleHisGlnAspSerPheLysGluArgAsnThrThrLeuValArg 818
 QY 2555 GAATTGGAGTAGCGCTGTGTGATCTGCTTACCTACCTATCGGATCCGATTGATGATG 2614
 Db 819 SerPheAspSerGlyAspLeuIleAsnValSerValProIleGlyIleThrPheGluArg 838
 QY 2615 GAATCAGACTGCCAGATCAAGTCAATCACTTGTGTTATCTGCTGATCTTGT 2674
 Db 839 PheSerArgAsnGluArgAlaSerTyrGluAlaThrValIleTyrValAlaAspValTyr 858
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 Db 859 ArgLysAsnProAspCysThrThrAlaLeuLeuIleAsnAsnThrSerTrpLysThrThr 878
 QY 2735 GGTAGCAATTTGGCAGACAGCTTTAGCTTCTGTCGTCAGGGAACCATTTTCTTAC 2794
 Db 879 GlyThrAsnLeuSerArgGlnAlaGlyIleGlyArgAlaGlyIlePheTyrAlaPheSer 898
 QY 2795 TCAAAATTTGAGCCCTTAGCCCAATTTCTTTGAATTCGTCGGGTCACTCGCAATTAC 2854
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 QY 2855 AATGTAGACTTAGAGCAAAATACCAATTC 2884
 Db 919 AsnAlaAspLeuGlyGlyLysPheGlnPhe 928
 RESULT 14
 ID AAY90239
 XX
 AC AAY90239;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Chlamydia antigen CPN100638.
 XX
 KW Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
 KW therapy; upper respiratory tract disease; bronchitis; sinusitis;
 KW asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.
 XX
 OS Chlamydia pneumoniae.
 XX
 PN W0200032794-A2.
 XX
 PD 08-JUN-2000.

XX 01-DEC-1999; 99WO-CA01147.
 XX 01-DEC-1998; 98US-0110339.
 PR 01-DEC-1998; 98US-0110340.
 PR 01-DEC-1998; 98US-0110427.
 PR 01-DEC-1998; 98US-0110428.
 PR 01-DEC-1998; 98US-0110438.
 PA (CONN-) CONNAUGHT LAB LTD.
 XX Murdin AD, Oomen RP, Wang J;
 PI WPI, 2000-412339/35.
 DR N-PSDB; AAA30851, AAA30852.
 DR
 PT Nucleic acids encoding polypeptide antigens from Chlamydia useful for
 PT preventing, diagnosing and treating diseases such as community acquired
 PT pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
 PT asthma -
 XX
 PS Claim 16; Fig 5; 17app; English.
 CC This sequence is a Chlamydia antigen of the invention, designated
 CC CPN100638. The nucleic acids (and their complementary sequences) may be
 CC used as diagnostic agents for detecting the presence of nucleic acids
 CC encoding Chlamydia antigens in samples according to standard methods,
 CC and therefore, for diagnosing Chlamydia infections. For example, they may
 CC be used as primers and probes for diagnostic polymerase chain reaction
 CC (PCR) assays. Antisense sequences may be used to down regulate
 CC expression of the proteins and may be used to treat infections. The
 CC nucleic acids may also be used to produce the protein antigens they
 CC encode according to standard recombinant DNA methodologies. The
 CC proteins may then be used as antigens for the production of antibodies
 CC (i.e. as vaccines) for preventing infection by Chlamydia. The
 CC antibodies may also be used as diagnostic reagents for detecting
 CC infections. Chlamydia is a pathogen implicated in the development of
 CC (for example) community acquired pneumonia, upper respiratory tract
 CC disease (especially bronchitis and sinusitis, asthmatic bronchitis,
 CC adult-onset asthma and acute exacerbations of asthma in adults.
 XX
 SQ Sequence 928 AA;
 Alignment Scores:
 Pred. No.: 7,04e-154 Length: 928
 Score: 1976.00 Matches: 428
 Percent Similarity: 60.84% Conservative: 150
 Best Local Similarity: 45.05% Mismatches: 328
 Query Match: 36.53% Indels: 44
 DB: 21 Gaps: 19
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 Db 1 MetLysSerSerLeuHisTrpPheLeuIleSerSerSerLeuAlaLeuProLeuSerLeu 20
 QY 161 -----ATTGCTACCGAGACAGCTTTTGGATTCAAGTCGCGAGTTTCGAT 202
 Db 21 AsnPheSerAlaPheAlaAlaValValGluIleAsnLeuGlyProThrAsnSerPheSer 40
 QY 203 GGGATAATAATGGTAATTTTTCAGTTCGTGAGAGTCAGGAAGATGCT---GGAACTACC 259
 Db 41 Gly-----ProGlyThrTyrThrProProAlaGlnThrThrAsnAlaAspGlyThrIle 58
 QY 260 TACTATTATTAAGGAAATGCTACTCTAGAAAATATTCTTGGAAACAGGACACAAATCACA 319
 Db 59 TyrAsnLeuThrGlyAspValSerIleThrAsn---AlaGlySerProThrAlaLeuThr 77
 QY 320 AAAAGCTGTTTAAACACACTAAGGCGGATTTGACTTTTACAGAGTTAACCGGAACTCTTA 379
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Db 799 ValGluAlaSerTyrIleHisGlnAspSerPheLysGluArgAsnThrThrLeuValArg 818
 Qy 2555 GAAATTTGAAGTAGCGCTTTGTGTAATCTGCCTTACCTATCGGATCCGATTTGATAAG 2614
 Db 819 SerPheAspSerGlyAspLeuIleAsnValSerValProIleGlyIleThrPheGluArg 838
 Qy 2615 GAATCAGACTGCCAAGATGCAAGTACAACTCACTCTGTTATCTACTGTGATCTTGT 2674
 Db 839 PheSerArgAsnGluArgAlaSerTyrGluAlaThrValIleTyrValAlaAspValTyr 858
 Qy 2675 CGTAGTACCCCGACTGTACGACACACTGCGAATTAGCGGTGATTTCTGGAACCTTC 2734
 Db 859 ArgLysAsnProAspCysThrThrAlaLeuLeuIleAsnAsnThrSerTyrLysThrThr 878
 Qy 2735 GGTACGAATTTGGCAAGCAAGCTTTAGTCTTCCTTCCTGCGAGCAACATTTTGTCTTAAC 2794
 Db 879 GlyThrAsnLeuSerArgGlnAlaGlyIleGlyArgAlaGlyIlePheTyrAlaPheSer 898
 Qy 2795 TCAAAATTTTGAAGCTTTAGCCAAATTTCTTTGTAATGCGGTGCTCATCTCGCAATTAC 2854
 Db 899 ProAsnLeuGluValThrSerAsnLeuSerMetGluIleArgGlySerSerArgSerTyr 918
 Qy 2855 AATGTAGACTTAGGAGCAAAATACCAATTC 2884
 Db 919 AsnAlaAspLeuGlyGlyLysPheGlnPhe 928
 RESULT 15
 AAY99842
 ID AAY99842 standard; Protein; 936 AA.
 AC AAY99842;
 XX
 DT 15-SEP-2000 (first entry)
 XX
 DE Chlamydia pneumoniae 98 kDa outer membrane protein CPN100640.
 XX
 KW Chlamydia; 98 kDa outer membrane protein; antigen; immunogen; infection;
 KW vaccine; antibacterial; community acquired pneumonia; bronchitis;
 KW sinusitis; acute respiratory disease; upper respiratory tract disease;
 KW asthma; atherosclerosis.
 XX
 OS Chlamydia pneumoniae.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..11
 FT Protein /label= Signal_peptide
 FT Protein 12..936
 FT Protein /label= 98_kDa_membrane_protein
 XX
 PN WO200032784-A1.
 XX
 PD 08-JUN-2000.
 XX
 XX 01-DEC-1999; 99WO-CA01148.
 XX
 XX 01-DEC-1998; 98US-0110439.
 PR 03-MAY-1999; 99US-0132272.
 XX
 XX (CONN-) CONNAUGHT LAB LTD.
 XX
 XX Murdin AD, Oomen RP, Wang J, Dunn P;
 XX WPI; 2000-412330/35.
 DR N-PSDB; AAA48838, AAA48839.
 XX
 XX New polynucleotide encoding the Chlamydia 98 kiloDalton outer membrane
 PT protein, useful for preventing or treating Chlamydia infection -
 PT
 XX Claim 16; Fig 1; 98pp; English.
 PS
 XX The present sequence is CPN100640, the 98 kDa outer membrane protein
 CC from Chlamydia pneumoniae. Chlamydia pneumoniae is a common cause of
 CC community acquired pneumonia and upper respiratory tract symptoms and

CC diseases, including bronchitis and sinusitis. It also has an association
 CC with atherosclerosis and asthma. The 98 kDa outer membrane protein is a
 CC C. pneumoniae-specific antigen which can confer immune protection against
 CC chlamydial infection. The nucleotide sequence encoding the protein or the
 CC protein itself may be administered as a vaccine to prevent or treat
 CC infection and they may also be used to diagnose infection. The gene
 CC encoding CPN100640 was amplified from Chlamydia pneumoniae genomic DNA
 CC by PCR.
 XX
 SQ Sequence 936 AA;
 Alignment Scores:
 Pred. No.: 5,68e-153 Length: 936
 Score: 1965.00 Matches: 411
 Percent Similarity: 62.30% Conservative: 179
 Best Local Similarity: 43.40% Mismatches: 327
 Query Match: 36.33% Indels: 30
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 Qy 158 ATGATTGCTACCGAGACAGATTTTGGATTCAAGT---GCGAGTTTTCGATGGGAATAAATAA 214
 Db 21 IleValAlaAlaGluValThrLeuAspSerSerAsnAsnSerTyrAspGlySerAsnGly 40
 Qy 215 GGTAAATTTTTCAGTTTCGTGAGAGTCAGGAA---GATGCTGGAACCTACCTACTATTTAAAG 271
 Db 41 ThrThrPheThrValPheSerThrThrAspAlaAlaGlyThrThrTyrSerLeuLeu 60
 Qy 272 GGAATGTCACTCTAGAAAAATATTCCTGGAAACAGCAGCAATCAACAAAAAGTGTTTT 331
 Db 61 SerAspValSerPheGlnAsnAlaGlyAlaLeuGlyIleProLeuAlaSerGlyCysPhe 80
 Qy 332 AACACACTAAGGCGGATTCACCTTTCACAGTACAGGGAACCTCTATTTGTTCCAAACG 391
 Db 81 LeuGluAlaGlyGlyAspLeuThrPheGlnGlyAsnGlnHisAlaLeuLysPheAlaPhe 100
 Qy 392 GTGATGACGAGGACTGTAGCAGGGGCTGCTGTTAAACAGCAGCGTGTAGATAAATCTACC 451
 Db 101 IleAsnAlaGlySerSerAlaGlyThrValAlaSerThrSerAlaAlaAspLysAsnLeu 120
 Qy 452 AGTTTATAGGTTTCTTCGCTATCTTTTATGCGTCTCTCTGGAAGTTCGATAACT--- 508
 Db 121 LeuPheAsnAspPheSerArgLeuSerIleIleSerCysProSerLeuLeuSerPro 140
 Qy 509 ACCGGCAAGGAGCGCTAGCTGCTACGGGTAGCTTGAGTTTCACAAAAAATCTCAGT 568
 Db 141 ThrGlyGlnCysAlaLeuLys---SerValGlyAsnLeuSerLeuThrGlyAsnSerGln 159
 Qy 569 TTGCTCTTCAGCAAAAACCTTTTCAACGGATATGCGGTGCTATCACCCGCAAAAACCTTT 628
 Db 160 IleIlePheThrGlnAsnPheSerSerAspAsnGlyGlyValIleAsnThrLysAsnPhe 179
 Qy 629 TCATTAAACAGGACTACAAATGTCAGCTCTGTTTCTGAAAATAAC-----TCCTCAAG 682
 Db 180 LeuLeuSerGlyThrSerGlnPheAlaSerPheSerArgAsnGlnAlaPheThrGlyLys 199
 Qy 683 AAAGCGGAGCCATTTCAGACTTCGATCCCTTACCTTACCTTACCTGGAACCAAGGGAAGTC 742
 Db 200 GlnGlyGlyValValThrAlaThrGlyThrIleThrIleGluAsnSerProGlyIleVal 219
 Qy 743 TCTTTTCTGCAATATCTTCTCGGATTCCTGAGTCTGCAATTTTACAGAACCTCGGTG 802
 Db 220 SerPheSerGlnAsnLeuAlaLysGlySerGlyGlyAlaLeuTyrSerThrAspAsnCys 239
 Qy 803 ACTATTTCTAATAGCTAAAGTTTCTTTTATGCAATAAGGTACAGGAGCGAGCTCC 862
 Db 240 SerIleThrAspAsnPheGlnValIlePheAspGlyAsnSerAlaTrpGluAlaGln 259

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 16, 2003, 10:21:34 ; Search time 27 Seconds
(without alignments)
9402.413 Million cell updates/sec

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Perfect score: 5409
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Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA.*

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2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 2997 | 55.4 | 597 | US-09-198-452A-29 | Sequence 29, Appl |
| 2 | 1940 | 35.9 | 930 | US-09-198-452A-470 | Sequence 470, App |
| 3 | 1917.5 | 35.5 | 927 | US-09-198-452A-472 | Sequence 472, App |
| 4 | 1871 | 34.6 | 949 | US-09-198-452A-478 | Sequence 478, App |
| 5 | 1572.5 | 29.1 | 643 | US-09-198-452A-474 | Sequence 474, App |
| 6 | 1417.5 | 26.2 | 922 | US-09-198-452A-15 | Sequence 15, Appl |
| 7 | 1264 | 23.4 | 671 | US-09-198-452A-468 | Sequence 468, App |
| 8 | 1214 | 22.4 | 230 | US-09-198-452A-30 | Sequence 30, Appl |
| 9 | 1204 | 22.3 | 507 | US-09-198-452A-32 | Sequence 32, Appl |
| 10 | 1130 | 20.9 | 1132 | US-09-198-452A-466 | Sequence 466, App |
| 11 | 1126.5 | 20.8 | 1006 | US-09-556-877-190 | Sequence 190, App |
| 12 | 1126.5 | 20.8 | 1006 | US-09-620-412C-190 | Sequence 190, App |

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| 13 | 1126.5 | 20.8 | 1006 | 4 | US-09-598-419-190 | Sequence 190, App |
| 14 | 1124.5 | 20.8 | 982 | 4 | US-09-556-877-176 | Sequence 176, App |
| 15 | 1124.5 | 20.8 | 982 | 4 | US-09-620-412C-176 | Sequence 176, App |
| 16 | 1124.5 | 20.8 | 982 | 4 | US-09-598-419-176 | Sequence 176, App |
| 17 | 1015.5 | 18.8 | 450 | 4 | US-09-198-452A-35 | Sequence 35, Appl |
| 18 | 888 | 16.4 | 530 | 4 | US-09-198-452A-482 | Sequence 482, App |
| 19 | 874 | 16.2 | 177 | 4 | US-09-198-452A-28 | Sequence 28, Appl |
| 20 | 865 | 16.0 | 880 | 4 | US-09-556-877-175 | Sequence 175, App |
| 21 | 865 | 16.0 | 880 | 4 | US-09-620-412C-175 | Sequence 175, App |
| 22 | 865 | 16.0 | 880 | 4 | US-09-598-419-175 | Sequence 175, App |
| 23 | 856 | 15.8 | 866 | 4 | US-09-556-877-189 | Sequence 189, App |
| 24 | 856 | 15.8 | 866 | 4 | US-09-620-412C-189 | Sequence 189, App |
| 25 | 856 | 15.8 | 866 | 4 | US-09-598-419-189 | Sequence 189, App |
| 26 | 842 | 15.6 | 483 | 4 | US-09-198-452A-27 | Sequence 27, Appl |
| 27 | 821 | 15.2 | 494 | 4 | US-09-198-452A-33 | Sequence 33, Appl |
| 28 | 792 | 14.6 | 427 | 4 | US-09-198-452A-31 | Sequence 31, Appl |
| 29 | 708 | 13.1 | 294 | 4 | US-09-198-452A-469 | Sequence 469, App |
| 30 | 680.5 | 12.6 | 1617 | 4 | US-09-198-452A-1035 | Sequence 1035, App |
| 31 | 667 | 12.3 | 1146 | 4 | US-09-198-452A-580 | Sequence 580, App |
| 32 | 650.5 | 12.0 | 969 | 4 | US-09-198-452A-501 | Sequence 501, App |
| 33 | 604.5 | 11.2 | 940 | 4 | US-09-198-452A-500 | Sequence 500, App |
| 34 | 582 | 10.8 | 1530 | 4 | US-09-556-877-178 | Sequence 178, App |
| 35 | 582 | 10.8 | 1530 | 4 | US-09-620-412C-178 | Sequence 178, App |
| 36 | 582 | 10.8 | 1530 | 4 | US-09-598-419-178 | Sequence 178, App |
| 37 | 559 | 10.3 | 1752 | 4 | US-09-556-877-180 | Sequence 180, App |
| 38 | 559 | 10.3 | 1752 | 4 | US-09-620-412C-180 | Sequence 180, App |
| 39 | 559 | 10.3 | 1752 | 4 | US-09-598-419-180 | Sequence 180, App |
| 40 | 546.5 | 10.1 | 964 | 4 | US-09-556-877-177 | Sequence 177, App |
| 41 | 546.5 | 10.1 | 964 | 4 | US-09-620-412C-177 | Sequence 177, App |
| 42 | 546.5 | 10.1 | 964 | 4 | US-09-598-419-177 | Sequence 177, App |
| 43 | 546.5 | 10.1 | 977 | 4 | US-09-556-877-191 | Sequence 191, App |
| 44 | 546.5 | 10.1 | 977 | 4 | US-09-620-412C-191 | Sequence 191, App |
| 45 | 546.5 | 10.1 | 977 | 4 | US-09-598-419-191 | Sequence 191, App |

ALIGNMENTS

RESULT 1
US-09-198-452A-29
; Sequence 29, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen
; thereof and uses thereof, in particular for the diagnosis, pre
; and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 29
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-29

Alignment Scores:
Pred. No.: 3.44e-256 Length: 597
Score: 2997.00 Matches: 596
Percent Similarity: 99.67% Conservative: 0
Best Local Similarity: 99.67% Mismatches: 1
Query Match: 55.41% Indels: 2
DB: 4 Gaps: 0

US-09-428-122-1 (1-3000) x US-09-198-452A-29 (1-597)

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| Qy | 604 | CGGTGCTATCACGCAAAAACCTTTTCATTAAACAGGACATACATGTCACCTCTGTTTC | 663 |
| Db | 20 | YGIYAlaIleThAlaIysThrLeuSerLeuThrGlyThrMetSerAlaLeuPheSe | 40 |

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QY 784 TTTTACAGAAGCCTCGGTGACTATTCTTAATAATCTAAAGTTTCTCTTTATATGCAATAA 843
Db 80 ePheThrGluAlaSerValThrIleSerAsnAsnAlaLysValSerPheIleAspAsnLys 100
QY 844 GGTCAAGAGAGAGCTCTCTCAACACGGGGATATGTCAGAGGTGCTATCTGTGCTTA 903
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Db 440 rThrAlaThrPheAsnTrpThrLysThrGlyTyIleProAsnProGluArgIleGlySe 460
QY 1924 TTTAGTCCCTAATAGCTATGGAATGATTTATAGATATTAGCTCTCTCCATTTATCTAT 1983
Db 460 rLeuValProAsnSerLeuTrpAsnAlaPheIleAspIleSerSerLeuHisTyLeuMe 480
QY 1984 GGAGACTGCAAAACCAAGGTTTGCAGGGAGACCGTGTCTTTTGGTGTGCTGGATTATCTAA 2043
Db 480 tGluThrAlaAsnGluGlyLeuGlnGlyAspArgAlaPheTrpCysAlaGlyLeuSerAs 500
QY 2044 CTTCTTCCATTAAGATAGTACAAAACACAGCGGGTTCGCCATTGAGTGGCGGTTA 2103
Db 500 nPhePheHisLysAspSerThrLysThrArgArgGlyPheArgHisLeuSerGlyTy 520
QY 2104 TGTCTAGAGAGAAACCTACATACTTGTTCAGATAAGATTCTTAGTGTGCTGCTATTGTCA 2163
Db 520 rValIleGlyGlyAsnLeuHisThrCysSerAspLysIleLeuSerAlaAlaPheCysG 540
QY 2164 GCTCTTTGGAAGATAGAGACTACTTTGTAGCTAAGAATCA-AGGTACAGTCTACGGAG 2222
Db 540 nLeuPheGlyArgAspArgAspTyPheValAlaLysAsnGlnArgTySerLeuArgAr 560
QY 2223 GAACCTCTATTACAGCACAAACCACTATATCTCTCTCTTCCCTGCAACTAGGCTT 2282
Db 560 sAsnSerLeuLeuProAlaGlnArgAsnLeuTyLeuSerSerLeuGlnThrThrAlaLe 580
QY 2283 GTTCGTTCTTATGTTCTCTACAGAGATTCTCTGTTCTCTTTTACGGAACCT 2334
Db 580 uPheValValLeuCysSerTyArgAspSerCysSerLeuPheArgLysPro 597

RESULT 2
US-09-198-452A-470
; Sequence 470, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme:
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr:
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 470
; LENGTH: 930
; TYPE: PR
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-470

Alignment Scores:
Pred. No.: 9,18e-163 Length: 930
Score: 1940.00 Matches: 416
Percent Similarity: 60.97% Conservative: 165
Best Local Similarity: 43.6% Mismatches: 324
Query Match: 35.8% Indels: 48
DB: 4 Gaps: 17

US-09-428-122-1 (1-3000) x US-09-198-452A-470 (1-930)
QY 101 ATGAAGTCTCTTCCCAAGTTTCTATTTCTACATTTGCTATTTTCCCTTGTCTATG 160
Db 1 MetLysIleProLeuHisLysLeuLeuIleSerSerThrLeuValThrProIleLeuLeu 20
```

QY 161 ---ATTGCTACC-----GAGACAGTTTTGGATTCAAGTCGCGAGTTTCGATCGGAAT 208
 Db 21 SerIleAlaThrTyrGlyAlaAspAlaSerLeuSerProThrAspSerPheAspGlyAla 40
 QY 209 AAAAATGGTAATTTTCAGTTCGTGAGAGTCAGGAAGATCGTGGAACTACTACCTACCTATT 268
 Db 41 GlyGlySerThrPheThrProLysSerThrAlaAspAlaAsnGlyThrAsnTyrValLeu 60
 QY 269 AAGGGAATCTACTCTAGAAATATTCCTGGACAGGCAAGCAATCACAAAAAGCTGT 328
 Db 61 SerGlyAsnValTyrIle---AsnAspAlaGlyLysGlyThrAlaLeuThrGlyCysCys 79
 QY 329 TTATAACAACACTAAGGCGATTTCATCTTCACAGGTAAACGGAACTCTCTATTGTTCCAA 388
 Db 80 PheThrGluThrThrGlyAspLeuThrPheThrGlyLysGlyTyrSerPheSerPheAsn 99
 QY 389 ACGGTGATCGAGGACTGTAGACGGGCTGCTGTTAAACAGCAGCGTGGTAGATAAATCT 448
 Db 100 ThrValAspAlaGlySerAsnAlaGlyAlaAlaAla---SerThrThrAlaAspLysAla 118
 QY 449 ACCAGTTTATAGGTTTCTCGCTATCTTTTATTCGCTCTCTCGTAAAGTTTCGATACT 508
 Db 119 LeuThrPheThrGlyPheSerAsnLeuSerPheIleAlaAlaProGlyThrThrValAla 138
 QY 509 ACCGGCAAGGAGCGGTAGCTGCTCTACGGGTAGCTTGAGTTTGACAAAATGTCAGT 568
 Db 139 SerGlyLysSerThrLeuSer---SerAlaGlyAlaLeuAsnLeuThrAspAsnGlyThr 157
 QY 569 TTGCTCTTCAGCAAAAATCTTTCAACCGAT-----AATGCGGTGCTATCACCGCA 619
 Db 158 IleLeuPheSerGlnAsnValSerAsnGluAlaAsnAsnAsnGlyGlyAlaIleThrAla 177
 QY 620 AAAACTCTTTCATTAACAGGACTACAAATGTAGCTCTGTTTCTGAAATACCTCTCTCA 679
 Db 178 LysThrLeuSerIleSerGlyAsnThrSerSerIleThrPheThrSerAsnSerAlaLys 197
 QY 680 AAGAAAGCGCGGCATTACAGCTTCGATCCGCTTACCATTACTGGAACCAAGGGGAA 739
 Db 198 LysLeuGlyGlyAlaIleTyrSerSerAlaAlaAlaSerIleSerGlyAsnThrGlyGln 217
 QY 740 GTCTCTTTTCTGCAATCTCTCTCGGATTCGAGCTGCAATTTTTCAGAAAGCTCTG 799
 Db 218 LeuValPheMetAsnAsnLysGlyGluThrGlyGlyAlaLeuGlyPheGluAlaSer 237
 QY 800 GTGCTATTCTTAATAGCTAAAGTTTCTTATTGACATAAGGTCACAGGAGCGAGC 859
 Db 238 SerSerIleThrGlnAsnSerSerLeuPhePheSerGlyAsnThrAlaThrAspAlaAla 257
 QY 860 TCCTCAACAACGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAACTAGTACAGAT 919
 Db 258 Gly-----LysGlyGlyAlaIleTyrCysGluLysThrGlyGluThr 271
 QY 920 ACTAAGGTCACTTCCTGGAATACAGATGTACTCTTCAGCAACAATACATCGACAACA 979
 Db 272 ProThrLeuThrIleSerGlyAsnLysSerLeuThrPheAlaGluAsnSerSerValThr 291
 QY 980 GCGGAGAGCTATCTATGTGAAAAGCTCGAATCGAATGCTCCGAGAGCTTACCTATTC 1039
 Db 292 GlnGlyGlyAlaIleCysAlaHisGlyLeuAspLeuSerAlaAlaGlyProThrLeuPhe 311
 QY 1040 AGTAGAATAGTGTCAATGGAGGTACAGCTCCTAAAGTGGAGGCATAGCTATCGAAGAT 1099
 Db 312 SerAsnAsnArGysGlyAsnThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAsp 331
 QY 1100 AGTGGGAATTCAGTTTATCCCGCATAGTGGTACATTTGCTTTTTCAGGAATACAGTC 1159
 Db 332 SerGlySerLeuSerLeuSerAlaAsnGlnGlyAspIleThrPheLeuGlyAsnThrLeu 351
 QY 1160 ACTTCTACTACT---CCTGGACGAATAGATAGTATCGACTTAGGAACGAGTGCAAG 1216
 Db 352 ThrSerThrSerAlaProThrSerThrArgAsnAlaIleTyrLeuGlySerSerAlaLys 371
 QY 1217 ATGACAGCTTTCGCTTCGTGCTGGTAGAGCCATCTACTTCTATGATCCCATATA----- 1270

Db 372 IleThrAsnLeuArgAlaAlaGlnGlyGlnSerIleTyrPheTyrAspProIleAlaSer 391
 QY 1271 ---ACTACAGATCATCCACAACAGTTACAGATGTCTTAAAAGTTAATGAGACTCCGGCA 1327
 Db 392 AsnThrThrGlyAlaSer-----AspValLeuThrIleAsnGlnProAspSer 407
 QY 1328 GATTCTGCACTCAATATACAGGACATCATCTTCACAGGAGAAAGTATCAGAGACA 1387
 Db 408 AsnSerProLeuAspTyrSerGlyThrIleValPheSerGlyGluLysLeuSerAlaAsp 427
 QY 1388 GAGGCCGAGATTCTTAAAAATCTTACTCGAAGCTACTACAGCCTCTAACTCTTTTCAGGA 1447
 Db 428 GluAlaLysAlaAlaAspAsnPheThrSerIleLeuLysGlnProLeuAlaLeuAlaSer 447
 QY 1448 GGTACTCTATCTTTAAAAACATGAGTACTCTGCAGACTCAGGCATCTCATCAACAGGCA 1507
 Db 448 GlyThrLeuAlaLeuLysGlyAsnValGluLeuAspValAsnGlyPheThrGlnThrGlu 467
 QY 1508 GATTCTCGTCTCGAAATGGACGTAGCAACTACTCTAGAACCTGCTGATACACCATATA 1567
 Db 468 GlySerThrLeuLeuMetGlnProGlyThrLysLeuLys---AlaAspThrGluAlaIle 486
 QY 1568 AAC-----AATTGCTCATTAACATCATCTTATAGACGGTGCAGGCAAGGCAAAATA 1621
 Db 487 SerLeuThrLysLeuValValAspLeuSerAlaLeuGluGlyAsnLysSerValSerIle 506
 QY 1622 GAAACCAAGCTAGCTCAAAAATCTGATCTTATCTGGAACCATCATCTTATTGGACCGC 1681
 Db 507 GluThrAlaGlyAlaAsnLysThrIleThrLeuSerProLeuValPheGlnAspSer 526
 QY 1682 ACGGGACGCTTTTATGAAATCATAGTTTAAAGAAATCCTCAGTCCTACGACATCTTAGAG 1741
 Db 527 SerGlyAsnPheTyrGluSerHisThrIleAsnGlnAlaPheThrGlnProLeuValVal 546
 QY 1742 CTCAAAAGCTTCT-----GGAACCTGTAAACAGCACCGCA 1774
 Db 547 PheThrAlaAlaThrAlaAlaSerAspIleTyrIleAspAlaLeuLeuThrSerProVal 566
 QY 1775 GTGACTCCAGATCCTATATGCGGTGAAATTCATTCAGGCTATCAGGAACTTGGGGC 1834
 Db 567 GlnThrProLupro-----HisTyrGlyTyrGlnGlyHisTyrGlu 580
 QY 1835 CCAATTCTTTGGGGACAGGGCTTCTACAGCTGCACCTTCACTGAGCTAAACCTGCGC 1894
 Db 581 AlaThrTrpAlaAspThrSerThrAlaLysSerGlyThrMetThrTrpValThrThrGly 600
 QY 1895 TATATTCTTAATCCCGAGCGTATCGGCTCTTATAGTCCCTAATAGCTTATGGAATCATTT 1954
 Db 601 TyrAsnProAsnProGluArgAlaSerValValProAspSerLeuTrpAlaSerPhe 620
 QY 1955 ATGATATTAGTCTCTCCATTTATCTTATGAGACTGCAACAGAGGTTGCGAGGAGAC 2014
 Db 621 ThrAspIleArgThrLeuGlnGlnIleMetThrSerGlnAlaAsnSerIleTyrGlnGln 640
 QY 2015 CGTGCTTTTGGGTGCTGATTTACTTCTTCCATAAGGATAGTACAAACACAGCA 2074
 Db 641 ArgGlyLeuTrpAlaSerGlyThrAlaAsnPhePheHisLysAspLysSerGlyThrAsn 660
 QY 2075 CGCGGGTTTCCCATTTGAGTGGCGGTATGTCTATAGGAGAAACCTTACATATCTTGTCA 2134
 Db 661 GlnAlaPheArgHisLysSerTyrGlyTyrIleValGlyGlySerAlaGluAspPheSer 680
 QY 2135 GATAAGATTTCTTGTGCTGCTATTTGTACCTCTTTCGAAAGAGATAGACTTCTTTGTA 2194
 Db 681 GluAsnIlePheSerValAlaPheCysGlnLeuPheGlyLysAspLysAspLeuPheIle 700
 QY 2195 GCTAAGATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCAGCAACAACCACTAT 2254
 Db 701 ValGluAsnThrSerHisAsnTyrLeuAlaSerLeuTyrLeuGlnHisArgAlaPheLeu 720
 QY 2255 ATCTCTCTTCTTCTGCAAACTACGGCCTTGT-----TCGTTGTCTTATGTTCTACAGAG 2308

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Db 721 GlyGlyLeuPro-----MetProSerPheGlySerIleThrAspMetLeuLysAsp 737
QY 2309 ATTCTGTCTCTTTTCCAGAAACCTTAGCTACACCCATACGGATACAGATCTGAAACCC 2368
Db 738 IleProLeuIleLeuAsnAlaGlnLeuSerTyrSerTyrThrLysAsnAspMetAspThr 757
QY 2369 AAGTATACAAATATCTTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAA 2428
Db 758 ArgTyrThrSerTyrProGluAlaGlnGlySerTrpThrAsnAsnSerGlyAlaLeuGlu 777
QY 2429 TTCGGTGAAGAGCTCCGATTTGCTTA--GATGAAGTCTCTATTGAGCAGTACATG 2485
Db 778 LeuGlyGlySerLeuAlaLeuLysLeuProLysGluAlaProPhePheGlnGlyTyrPhe 797
QY 2486 CCTTTCATGAAATTGTCAGTTGTCTATGCATCAGGAAGGTTTAAAGACAGGGAACA 2545
Db 798 ProPheLeuLysPheGlnAlaValTyrSerArgGlnGlnAsnPheLysGluSerGlyAla 817
QY 2546 GAAGTCGTGAAATTGGGAAGTAGCCGCTCTGTGTAATCTTGCTTACCTATCGGATCCGA 2605
Db 818 GluAlaArgAlaPheAspAspGlyAspLeuValAsnCysSerIleProValGlyIleArg 837
QY 2606 TTTGATAGGAATCAGACTGCCAAGATCAACGTACAATCTTAACCTCTTGGTTATACTGTG 2665
Db 838 LeuGluLysIleSerGluAspGluLysAsnAsnAsnPheGluIleSerLeuAlaTyrIleGly 857
QY 2666 GATCTTGTTCGTAGTAACCCGACTGTACGACACACATCGCAATTAGCGGTGATTCCTGG 2725
Db 858 AspValTyrArgLysAsnProArgSerArgThrSerLeuMetValSerGlyAlaSerTrp 877
QY 2726 AAAACCTTCGGTACGAATTTGCAAGACAGCTTAGTCTTCCTCGTGCAGGGAACCATTTT 2785
Db 878 ThrSerLeuCysLysAsnLeuAlaArgGlnAlaPheLeuAlaSerAlaGlySerHisLeu 897
QY 2786 TCGTTTAACCTCAAATTTGAACCTTTAGCCCAATTTCTTTGAATTCGTCGGGTCACTC 2845
Db 898 ThrLeuSerProHisValGluLeuSerGlyGluAlaAlaTyrGluLeuArgGlySerAla 917
QY 2846 CGCAATTAATGATGACTTAGGACAAATACCAATTC 2884
Db 918 HisIleTyrAsnValAspCysGlyLeuArgTyrSerPhe 930

RESULT 3
US-09-198-452A-472
; Sequence 472, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 472
; LENGTH: 927
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...927
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-472

Alignment Scores:
Pred. No.: 8,89e-161 Length: 927
Score: 1917.50 Matches: 427
Percent Similarity: 60.23% Conservative: 147
Best Local Similarity: 44.81% Mismatches: 328
Query Match: 35.45% Indels: 51
DB: 4 Gaps: 22
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US-09-428-122-1 (1-3000) x US-09-198-452A-472 (1-927)
QY 101 ATGAAGTCTTTTCCCAAGTTTGTATTTCTTACATTTGCTATTTTCCCTTTGTCTATG 160
Db 1 MetLysSerSerLeuHisTrpPheLeuIleSerSerLeuAlaLeuProLeuSerLeu 20
QY 161 -----ATTGTCACCGACAGCTTTTGGATTCAAGTCGCGAGTTTCGAT 202
Db 21 AsnPheSerAlaPheAlaValAlaValGluIleAsnLeuGlyProThrAsnSerPheSer 40
QY 203 GGGAAATAAAATGTAATTTTTCAGTTTCGTGACAGTTCAGGAAGATGCT--GGAACCTACC 259
Db 41 Gly-----ProGlyThrTyrThrProProAlaGlnThrThrAsnAlaAspGlyThrIle 58
QY 260 TACCTATTTAAGGGAATGTCACCTCTAGAAAATATCTCTGGAACAGCAGCAATCACA 319
Db 59 TyrAsnLeuThrGlyAspValSerIleThrAsn---AlaGlySerProThrAlaLeuThr 77
QY 320 AAAAGCTGTTTAAACACACTAAGGCGGATTGTGACTTTTCACAGTAAACGGAACTCTCTA 379
Db 78 AlaSerCysPheLysGluThrThrGlyAsnLeuSerPheGlnGlyHisGlyTyrGlnPhe 97
QY 380 TTGTTTCCAAAACGCTGATGACAGGACTGTAGCAGGGGCTGCTGTTAAACAGCAGCGTGGTA 439
Db 98 LeuLeuGlnAsnIleAspAlaGly-----AlaAsnCysThrPheThrAsnThrAlaAla 115
QY 440 GATAAATCTACACGTTTATAGGTTTCTTCGGTATCTCTTATTTATGCTGCTCCTGGAGT 499
Db 116 AsnLysLeuLeuSerPheSerGlyPheSerTyrLeuSerLeuIleGlnThr-----Thr 133
QY 500 TCGATAACTACCGCAAGGAGCGGTAGCTGCTACGGGTAGCTGAGTTTCAGTAAACAAAA 559
Db 134 AsnAlaThrThrGlyThrGlyAlaIleLys---SerThrGlyAlaCysSerIleGlnSer 152
QY 560 AATGTCAGTTTGTCTCTTCAGCAAAAACCTTTTCAACGGATAATGCGGTGCTATCACCGCA 619
Db 153 AsnTyrSerCysTyrPheGlyGlnAsnPheSerAsnAspAsnGlyGlyAlaLeuGlnGly 172
QY 620 AAAACTCTTTCATTAACAGGAGCTACATGTGCTGCTGTTTCTGAAAATACCTCCTCA 679
Db 173 SerSerIleSerLeuSer---LeuAsnProAsnLeuThrPheAlaLysAsnLysAlaThr 191
QY 680 AAGAAAGCGCGGACCATTCAGACTTCGATCCCTTACCATTACTGGAACCAACGAGGAA 739
Db 192 GlnLysGlyGlyAlaLeuTyrSerThrGlyGlyIleThrIleAsnAsnThrLeuAsnSer 211
QY 740 GTCTCTTTTCTGCAATATCTTCTCGGATCTCGAGCTGCAATTTTACAGAGCCTCG 799
Db 212 AlaSerPheSerGluAsnThrAlaAlaAsnAsnGlyGlyAlaIleTyrThrGluAlaSer 231
QY 800 GTGACTATTTCTTAATGCTAAAGTTTCCCTTATTGACAATAGTTCACAGGACGAGC 859
Db 232 SerPheIleSerSerAsnLysAlaIleSerPheIleAsnAsnSerValThrAlaThrSer 251
QY 860 TCCTCAACACACGGGGGATATGTACGAGGTGCTATCTGCTTATATAAAATAGTACAGAT 919
Db 252 Ala-----ThrGlyAlaIleTyrCysSerSerThrSerAlaPro 265
QY 920 ACTAAGTTC---ACCCTCACTGGAATCAGATGTTTACTCTTCAGCAACAATACATPCGACA 976
Db 266 LysProValLeuThrLeuSerAspAsnGlyGluLeuAsnPheIleGlyAsnThrAlaIle 285
QY 977 ACAGCGGAGGAGCTATCTATGTGAAAAGCTGCAACTGGCTTCGGGAGGACTTACCCTA 1036
Db 286 ThrSerGlyGlyAlaIleTyrThrAspAsnLeuValLeuSerSerGlyGlyProThrLeu 305
QY 1037 TTCAGTAGAATAGTGTCAATGGAGGTACAGCTCCCTAAAGTGGAGCCATAGTATCGAA 1096
Db 306 PheLysAsnAsnSerAlaIleAspThrAlaAlaProLeuGlyGlyAlaIleAlaIleAla 325
QY 1097 GATAGTGGGGAATGAGTTTATCCCGCGATAGTGTGACATTGCTTTTATGGGGAATACA 1156
Db 326 AspSerGlySerLeuSerLeuSerAlaLeuGlyGlyAspIleThrPheGluGlyAsnThr 345
```

| | | | | |
|----|------|--|--|------|
| QY | 1157 | GTC----- | ACTTCTACTCTCTCGCAGCAATAGAAAGTAGTAGTATCGACTTAGCA--- | 1204 |
| Db | 346 | ValVallyysGlyAlaSerSerGlnThrThrArgAsnSerIleAsnIleGlyAsn | 365 | |
| QY | 1205 | ACGAGTCAAGAATGACAGCTTTGCGTTCGCTGCTGGTAGAGCCATCTACTTCTATGAT | 1264 | |
| Db | 366 | ThrAsnAlaIysIleValGlnLeuArgAlaSerGlnGlyAsnThrIleTyrPheTyrAsp | 385 | |
| QY | 1265 | CCCATAACTACAGATCATCCACAACAGTTACAGATGCTCTAAAGTTTAAATGAGACTCCG | 1324 | |
| Db | 386 | ProIleThrThrSerIleThrAlaAlaLeuSerAspAlaLeuAsnLeuAenGlyProAsp | 405 | |
| QY | 1325 | GCAGATTCTGCACATAACATACAGGAAACATCATCTTCCAGGAGAAAAGTTATCAGAG | 1384 | |
| Db | 406 | LeuAlaGlyAsnProAlaTyrGlnGlyThrIleValPheSerGlyGluLysLeuSerGlu | 425 | |
| QY | 1385 | ACAGAGCCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCGCTGTAATCTTTTCA | 1444 | |
| Db | 426 | AlaGluAlaAlaGluAlaAspAsnLeuLysSerThrIleGlnGlnProLeuThrLeuAla | 445 | |
| QY | 1445 | GGAGGTACTCTATCTTTAAACATGGAGTGACTCTGCAGACTCAGGCAITTCACCTACACAG | 1504 | |
| Db | 446 | GlyGlyGlnLeuSerLeuLysSerGlyValThrLeuValAlaLysSerPheSerGlnSer | 455 | |
| QY | 1505 | GCAGATTCTCTCTCGAAATCGACTAGGAATCTACTCTAGAACCCTGCTGATACTGACCC | 1564 | |
| Db | 466 | ProGlySerThrLeuLeuMetAspAlaGlyThrThrLeuGluThrAlaAspGlySer--- | 484 | |
| QY | 1565 | ATAACCAATTTGGTCATTAAACATCAGTTCTATAGACGGTGCAAGAGGCAAAATAGAA | 1624 | |
| Db | 485 | -----LeuSerIleIleCysSerGlnCysArgPheLeuLysArgAspGlnGlu** | 501 | |
| QY | 1625 | ACC---AAAGCTACG----- | 1675 | |
| Db | 502 | ThrLeuLysAlaThrGlnAlaSerGlnThrValThrLeuSerGlySerLeuSerLeuVal | 521 | |
| QY | 1676 | GACCGACGGGCACGTTTATGAAATCATAGTTTAAAGAAATCTCTAGTCTCTACACATC | 1735 | |
| Db | 522 | AspProSerGlyAsnValTyrGluAspValSerTrpAsnAsnProGlnValPheSerCys | 541 | |
| QY | 1736 | TTAGAGCTCAAGCTTCT------ | 1789 | |
| Db | 542 | LeuThrLeuThrAlaAspAspProAlaAsnIleHisIleThrAspLeuAlaAlaAspPro | 561 | |
| QY | 1790 | ATAATGGGTGAAATTCATTACGGCTATCAGGGAACCTGGGCCCAATGTTTGGGGG | 1849 | |
| Db | 562 | LeuGluLysAsnProIleHisTrpGlyTyrGlnGlyAsnTrpAla---LeuSerTrpGln | 580 | |
| QY | 1850 | ACAGGGGCTCTACG----- | 1900 | |
| Db | 581 | GluAspThrAlaThrLysSerLysAlaAlaThrLeuThrTrpThrLysThrGlyTyrAsn | 600 | |
| QY | 1901 | CCTAATCCCGACGCTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGAT | 1960 | |
| Db | 601 | ProAsnProGluArgGlyThrLeuValAlaAsnThrLeuTrpGlySerPheValAsp | 620 | |
| QY | 1961 | ATTAGCTCTCCATATCTTATGGAGACTGCAACAGAGGGTTGACGGGACCGTGCT | 2020 | |
| Db | 621 | ValArgSerIleGlnGlnLeuValAlaThrLysValArgGlnSerGlnGluThrArgGly | 640 | |
| QY | 2021 | TTTTCGGTGTGCGATTATCTAACTCTTCCATAGGATAGTACAAAACACGACGGGG | 2080 | |
| Db | 641 | IleTrpCysGluGlyIleSerAsnPhePheLysAspSerThrLysIleAsnLysGly | 660 | |
| QY | 2081 | TTTTCGCCATTTTCAGTGGCGGTTGATGTCATAGGAGGAAACCTACATACCTGTGTCAGATAAG | 2140 | |
| Db | 661 | PheArgHisIleSerAlaGlyTyrValValGlyAlaThrThrThrLeuAlaSerAspAsn | 680 | |
| QY | 2141 | ATTCTTAGTGTGCATTTTGTGTCAGCTCTTTGGAAGAGATAGACTACTTTGTAGCTAAG | 2200 | |
| Db | 681 | LeuIleThrAlaAlaPheCysGlnLeuPheGlyLysAspArgAspHisPheIleAsnLys | 700 | |

[illegible]

| | | | |
|------------------------|---------|---------------|-----|
| Score: | 1871.00 | Matches: | 413 |
| Percent Similarity: | 60.49% | Conservative: | 175 |
| Best Local Similarity: | 42.49% | Mismatches: | 334 |
| Query Match: | 34.59% | Indels: | 50 |
| DB: | 4 | Gaps: | 22 |

| | | | |
|---|-----|--|------|
| US-09-428-122-1 (1-3000) x US-09-198-452A-478 (1-949) | | | |
| QY | 50 | TTGGTGATCTCTTAAATAATTAATT-----CAAAATCAAAGTATA | 91 |
| DB | 1 | LeuIleThrLeuPheCysPheThrIleAspAlaSerSerLeuLysAsnLysSerIle | 20 |
| QY | 92 | TATTTTACAATCAAGTCTCTTCCCAAGTTGTATTTCTACATTTGCTATTTCCT | 151 |
| DB | 21 | -----ThrMetLysThrSerIleProThrValLeuValSerValLeuAlaPheSer | 38 |
| QY | 152 | -----TTGCTATGATTTACCGAGACAGTTTGGATTCAAGTGGAGTTTCGATGG | 205 |
| DB | 39 | CysHisLeuGlnSerLeuAlaAsnGluLeuLeuSerProAspSerPheAsnGly | 58 |
| QY | 206 | AAT---AAAAATGGTAATTTTTCAGTTCGTGAGACTCAGGAAGATGCTGGAACCTAC | 262 |
| DB | 59 | AsnIleAspSerGlyThrPheThrProLysThrSer-----AlaThrThrTyr | 74 |
| QY | 263 | CTATTTAAGGGAATGTCACCTCTAGAAATATTCCTGAAACAGGCACAGCAATC | 322 |
| DB | 75 | SerLeuThrGlyAspValPhePheTyrGlu---ProGlyLysGlyThrProLeuSerAsp | 93 |
| QY | 323 | AGCTTTTAAACACACTAAGGCGATTTGACTTTCACAGGTAACGGGAATCTCTATTG | 382 |
| DB | 94 | SerCysPheLysGlnThrThrAspAsnLeuThrPheLeuGlyAsnGlyHisSerLeuThr | 113 |
| QY | 383 | TTCCAAACCGTGGATGTCAGGACTCTAGCAGGGGTGCTTTAAACAGCAGCGTGTAGAT | 442 |
| DB | 114 | PheGlyPheIleAspAlaGlyThrHisAlaGlyAlaAlaA---SerThrThrAlaAsn | 132 |
| QY | 443 | AAATCTACACGTTTATAGGTTTCTTCGCTATCTTTTATTTGCTCTCTCGGAAGTTCG | 502 |
| DB | 133 | LysAsnLeuThrPheSerGlyPheSerLeuLeuSerPheAspSerProSerThrThr | 152 |
| QY | 503 | ATACTACCGGCAAGGACCGTTAGTCTCTACGGGTAGCTTGAGTTTGACAAAAAT | 562 |
| DB | 153 | ValThrThrGlyGlnGlyThrLeuSer---SerAlaGlyGlyValAsnLeuGluAsnIle | 171 |
| QY | 563 | GTCAAGTTTCTCTCAGCAAAATCTTCAACGGGATAATGGCGTCTATCACCGCAAA | 622 |
| DB | 172 | ArgLysLeuValValAlaGlyAsnPheSerThrAlaAspGlyGlyAlaIleLysGlyAla | 191 |
| QY | 623 | ACTTTTCAATTAACAGGACTCAATGTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT | 682 |
| DB | 192 | SerPheLeuLeuThrGlyThrSerGlyAspAlaLeuPheSerAsnAsnSerSerThr | 211 |
| QY | 683 | AAAGCGGAGCATTCAGACTCCGATCCGATTCATCCATTAAGTGAACCAAGGGAAGTC | 742 |
| DB | 212 | LysGlyGlyAlaIleAlaThrThrAlaGlyAlaArgIleAlaAsnAsnThrGly***Val | 231 |
| QY | 743 | TCTTTTCTCAATACTCTCTCGGATTTCTGGAGCTGCAATTTTACAGAGCCTCGGTG | 802 |
| DB | 232 | ArgPheLeuSerAsnIleAlaSerThrSerGlyGlyAlaIleAspAspGluGlyThrSer | 251 |
| QY | 803 | ACTATTCTTAATGCTAAGTTTCTCTGATTTGACAAATAGTCTACAGGAGGAGCTCC | 862 |
| DB | 252 | IleLeuSerAsnAsnLysPheLeuTyrPhe-----GluGlyAsnAlaAla | 266 |
| QY | 863 | TCACACAGGGGATATGTCTGAGGAGTCTATCTGTCTTATATAAATAGTACAGATACT | 922 |
| DB | 267 | LysThrThr-----GlyGlyAlaIleCysAsnThrLysAlaSerGlySerPro | 282 |
| QY | 923 | AAGTCTACCTCACTGAAATCAGATCTTACTCTTTCAGCAACAATATCATCAACAGCG | 982 |
| DB | 283 | GluLeuIleIleSerAsnAsnLysThrLeuIlePheAlaSerAsnValAlaGluThrSer | 302 |
| QY | 983 | GGAGGAGCTATCTATGTGAAAAAGCTCGAACTGCTCCGGAGGACTTACCTATTTCAGT | 1042 |

| | | | |
|----|------|---|------|
| DB | 303 | GlyGlyAlaIleHisAlaLysLysLeuAlaLeuSerSerGlyGlyPheThrGluPheLeu | 322 |
| QY | 1043 | AGAAATAGTGTCAATGGAGGTACAGCTCTCTAAAGGTGGAGCCATAGCTATCGAAGATAGT | 1102 |
| DB | 323 | ArgAsnAsnValSerSerAlaThr---ProLysGlyGlyAlaIleSerIleAspAlaSer | 341 |
| QY | 1103 | GGGAATGAGTTTATCCGCCGATAGTGGTGACATTTGCTTTTGGGATATCAGTCACCT | 1162 |
| DB | 342 | GlyGluLeuSerLeuSerAlaGluThrGlyAsnIleThrPheValArgAsnThrLeuThr | 361 |
| QY | 1163 | TCTACT-----ACTCTGGGACCAATAGAAAGTATGACATTCAGCTTAGCAACGAGTGA | 1216 |
| DB | 362 | ThrThrGlySerThrAspThrProLysArgAsnAlaIleAsnIleGlySerAsnGlyLys | 381 |
| QY | 1217 | ATGACAGCTTTGGTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT | 1276 |
| DB | 382 | PheThrGluLeuArgAlaAlaLysAsnHisThrIlePhePheTyrAspProIleThr--- | 400 |
| QY | 1277 | GGATCATCCACAGTTACAGATGCTTAAAGTTAATGAGACTCCGGCAGATTCTGTCA | 1336 |
| DB | 401 | ---SerGluGlyThrSerSerAspValLeuLysIleAsnAsnGlySerAlaGlyAlaLeu | 419 |
| QY | 1337 | CTACAATATACAGGGAACATCATCTTCACAGGAGAAAAGTTATCAGACAGAGCGCGCA | 1396 |
| DB | 420 | AsnProLysGlnGlyThrIleLeuPheSerGlyGluThrLeuThrAlaAspGluLeuLys | 439 |
| QY | 1397 | GATTTAAAATCTTACTTCGAACTACTACAGCTGTAACTCTTTTTCAGAGGAGTACTCTA | 1456 |
| DB | 440 | ValAlaAspAsnLeuLysSerSerPheThrGlnProValSerLeuSerGlyGlyLysLeu | 459 |
| QY | 1457 | TCTTTAAAACATGAGTGTCTCTCAGACTCAGGACTCTCAACAGGAGATTTCTCGT | 1516 |
| DB | 460 | LeuLeuGlnLysGlyValThrLeuGluSerThrSerPheSerGlnGluAlaGlySerLeu | 479 |
| QY | 1517 | CTCGAATGAGAGTAGGAATCTACTCTAGAA---CCTGTGTATCTAGCACCAATAACAAT | 1573 |
| DB | 480 | LeuGlyMetAspSerGlyThrLeuSerThrThrAlaGlySerIleThrIleThrAsn | 499 |
| QY | 1574 | TGCTCATTAATCATCAGTTCTATAGCGTCAAGGTCGCAAGAGGCAAAATAGAACCAAGCT | 1633 |
| DB | 500 | LeuGlyIleAsnValAspSerLeuGlyLeuLysGlnProValSerLeuThrAlaLysGly | 519 |
| QY | 1634 | ACGTCAAAATCTGACTTTTATCGAACCATCATCTTTATTTGGACCGCAGCGGACGTTT | 1693 |
| DB | 520 | AlaSerAsnLysValIleValSerGlyLysLeuAsnLeuIleAspIleGluGlyAsnIle | 539 |
| QY | 1694 | TATGAAAAATCATAGTTTAAAGAAATCTCAGTCTCTACGACATCTTTAGAGCTCAAAGCTTCT | 1753 |
| DB | 540 | TyrGluSerHisMetPheSerHisAspGlnLeuPheSerLeuLeuLysIleThrValAsp | 559 |
| QY | 1754 | GGAACTGTAAACAAGC-----ACCGAGTGTACTCCAGATCTCTATATATGCGGTGAG | 1801 |
| DB | 560 | AlaAspValAspThrAsnValAspIleSerLeuIleProValProAlaGluAspPro | 579 |
| QY | 1802 | AAATTCATTCAGGCTATCAGGAACTTGGGCGCCCAATTTGTTGGGACAGGGGCTTCT | 1861 |
| DB | 580 | AsnSerGluTyrGlyPheGlnGlyGlnThrPheAsn---ValAsnThrThrThrAspThrAla | 598 |
| QY | 1862 | ACGACT-----GCAACCTTCAACTGGACTAAACCTGGCTATATTTCTTAATCCCGAG | 1912 |
| DB | 599 | ThrAsnThrLysGluAlaThrAlaThrThrLysThrGlyPheValProSerProGlu | 618 |
| QY | 1913 | CGTATCGGCTCTTATAGTCCCTAATAGCTATGGAATGCAATTTATAGATATAGTCTCTC | 1972 |
| DB | 619 | ArgLysSerAlaLeuValCysAsnThrLeuThrGlyValPheThrAspIleArgSerLeu | 638 |
| QY | 1973 | CATTATCTTATGAGACTCAACACGAGGTGTCAGGAGACCGGTCTTTTGGTGTGCT | 2032 |
| DB | 639 | GlnGlnLeuValGluIleGlyAlaThrGlyMetGluHisLysGlnGlyPheThrValSer | 658 |
| QY | 2033 | GGATTATCTAACTTCTTCCATAGGATAGTACAAACCAACGACGCGGGTTTCGCCATTTG | 2092 |

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Db 659 SerMetThrAsnPheLeuHisLysThrGlyAspGluAsnArgLysGlyPheArgHisThr 678
Qy 2093 AGTGGCGGTATGTATAGAGGAACCTACATCTTGTTCAGATAAGATCTTGTAGTCT 2152
Db 679 SerGlyGlyTyrValIleGlySerAlaHisThrProLysAspLeuPheThrPhe 698
Qy 2153 GCATTTTGTACCTCTTGGAGAGATAGAGACTACTTGTAGTAAAGATCAAGGTACA 2212
Db 699 AlaPheCysHisLeuPheAlaArgAspLysAspCysPheIleAlaHisAsnAsnSerArg 718
Qy 2213 GTCTACGAGGAACTCTATTACAGCAGCAACAGAAACC-----TATATC 2257
Db 719 ThrTyrGlyGlyThrLeuPhePheLysHisSerHisThrLeuGlnProGlnAsnTyrLeu 738
Qy 2258 TCTCTT---CCTTGCAACTACGGCTCTGTTCTGTCTTATGTTCCTACAGAGATTCCT 2314
Db 739 ArgLeuGlyArgAlaLysPheSerGluSerAlaIleGluLysPheProArgGluIlePro 758
Qy 2315 GTTCTCTTTTCAGAAACCTTAGCTACACCCATACGGATAACGATCTGAAACCAAGTAT 2374
Db 759 LeuAlaLeuAspValGlnValSerPheSerHisSerAspAsnArgMetGluThrHisTyr 778
Qy 2375 ACAACATATCTACTCTTAAAGAAAGCTGGGGAATGATAGTTTCGCTTTAGAAATTCGGT 2434
Db 779 ThrSerLeuProGluSerGluGlySerTrpSerAsnGluCysLeuAlaGlyIleGly 798
Qy 2435 GGAAGAGCTCGATTTGGCTTA---GATGAAAGTGTCTATTATGACAGATACATGCCCTC 2491
Db 799 LeuAspLeuProPheValLeuSerAsnProHisProLeuPheLysThrPheIleProGln 918
Qy 2492 ATCAATTCGACTTCTCTATGCATCAGCAGGATTTTAAAGAACAGGGAACAGAGCT 2551
Db 819 MetLysValGluMetValTyrValSerGlnAsnSerPhePheGluSerSerSerArg 938
Qy 2552 CGTGAATTTGGAAGTAGCGCTCTTGGAATCTTGCTTACCTATCGGGATCCGATTTGAT 2611
Db 839 ArgGlyPheSerIleGlyArgLeuLeuAsnLeuSerIleProValGlyAlaLysPhe--- 857
Qy 2612 AAGGAATCAGATGCCAAGATGCA---ACGTACAATCTTAACCTTGGTTATATCTGTGGAT 2668
Db 858 ValGlnGlyAspIleGlyAspSerTyrThrTyrAspLeuSerGlyPheValSerAsp 877
Qy 2669 CTGTGCTAGTAAACCCGACTCTACACACACTCGGATGCGATGATCTTCGGAA 2728
Db 878 ValTyrArgAsnAsnProGlnSerThrAlaThrLeuValMetSerProAspSerTrpLys 897
Qy 2729 ACCTTCGTAACGAATTTGCAAGACAGCTTTAGTCCTTCGTGACGGGAACCAATTTTGC 2788
Db 898 IleArgGlyGlyAsnLeuSerArgGlnAlaPheLeuLeuArgGlySerAsnAsnTyrVal 917
Qy 2789 TTAACTCAATTTTGAAGCTTTTAGCCATTTTCTTTTGAATTTGGTGGTGCATCTCGC 2848
Db 918 TyrAsnSerAsnCysGluLeuPheGlyHisTyrAlaMetGluLeuArgGlySerSerArg 937
Qy 2849 AATTCAATCTAGACTAGCAGCAATCAATCAATTC 2884
Db 938 AsnTyrAsnValAspValGlyThrLysLeuArgPhe 949
```

RESULT 5

```
US-09-198-452A-474
; Sequence 474, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 474
; LENGTH: 643
```

```
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-474
Alignment Scores:
Pred. No.: 2,2e-130 Length: 643
Score: 1572.50 Matches: 314
Percent Similarity: 64.50% Conservative: 93
Best local Similarity: 49.76% Mismatches: 209
Query Match: 29.07% Indels: 15
DB: 4 Gaps: 6
US-09-428-122-1 (1-3000) x US-09-198-452A-474 (1-643)
Qy 1022 GGAGACTTACCCCTTATTCAGTAGAATAGTGTCAATGAGGAGTACAGCTCCTTAAGGTGGA 1081
Db 18 GlyGlyGlyIleSerPheSerAsnAsnIleValGlnGlyThrThrAlaGlyAsnGlyGly 37
Qy 1082 GCATAGCTATTCGAAAGATAGTGGGAAATTGAGTTTATCCGCGATAGTGGTGACATTGTC 1141
Db 38 AlalIleSerIleLeuAlaAlaGlyGlyCysSerLeuSerAlaGluAlaGlyAspIleThr 57
Qy 1142 TTTTTAGGGAATPACAGTCACTTCTACTACTCT---GGGACGAATAGAGTAGTAGTACGAC 1198
Db 58 PheAsnGlyAsnAlaIleValAlaThrThrProGlnThrThrLysArgAsnSerIleAsp 77
Qy 1199 TTAGGAACGAGTGCAGGATGACAGCTTTGCTTCTGCTGCTGCTGCTAGAGCCATCTACTTC 1258
Db 78 IleGlySerThrAlaLysIleThrAsnLeuArgAlaIleSerGlyHisSerIlePhePhe 97
Qy 1259 TATGATCCCATAACTACAGGATCATCCACAGTTACAGATGTCTTAAAGCTTAATGAG 1318
Db 98 TyrAspProIleThrAlaAsnThrAlaAlaAspSerThrAspThrLeuAsnLeuAsnLys 117
Qy 1319 ACTCGGCGAGATTCGCACTACAATATATACAGGAACATCATCTTCACAGGAGAAAGTTA 1378
Db 118 AlaAspAlaGlyAsnSerThrAspTyrSerGlySerIleValPheSerGlyGlyLysLeu 137
Qy 1379 TCAGAGACAGAGCGCGAGATTTCTAAATCTTACTTCGAACTACTACAGCTGTAACT 1438
Db 138 SerGluAspGluAlaLysValAlaAspAsnLeuThrSerThrLeuLysGlnProValThr 157
Qy 1439 CTTTCAGGAGGTACTCTATCTTTTAAACATGAGTACTCTCGAGCTCAGACTCAGGCATTCACT 1498
Db 158 LeuThrAlaGlyAsnLeuValLeuLysArgGlyValThrLeuAspThrLysGlyPheThr 177
Qy 1499 CAACAGGCGAGATTCGCTCGAAATGGACGAGGAGGAGTACTCTAGAACCTGCT---GAT 1555
Db 178 GlnThrAlaGlySerSerValIleMetAspAlaGlyThrThrLeuLysAlaSerThrGlu 197
Qy 1556 ACTGACCACTAAACAAATTTGGTCTTAACTACATCAGTTCTATAGACGGTCAAGAGGCA 1615
Db 198 GluValThrLeuThrGlyLeuSerIleProValAspSerLeuGlyGlyLysVal 217
Qy 1616 AAAATAGAACCAACAGCTACGTCAAAAATCTGACTTTTATCTGGAACCACTCACTTTATTG 1675
Db 218 ValIleAlaAlaSerAlaAlaSerLysAsnValAlaLeuSerGlyProIleLeuLeuLeu 237
Qy 1676 GACCCGACGGCAGCGTTTATGAAATCATAGTTTAAAGAAATCCTCAGTCTCAGCAGCATC 1735
Db 238 AspAsnGlnGlyAsnAlaTyrGluAsnHisAspLeuGlyLysThrGlnAspPheSerPhe 257
Qy 1736 TTAGAGCTCAAGCTCTCGAACTGTAAACAGCAGCGAGTACTCCAGATCCTATAATG 1795
Db 258 ValGlnLeuSerAlaLeuGlyThrAlaThrThrThrAspValProAlaValProThrVal 277
Qy 1796 GGTGAGAAATTCATTACCGCTATCAGGAACTTGGGCCCAATCTTTGG----- 1846
Db 278 AlaThrProThrHisTyrGlyThrGlnGlyThrTrpGly---MetThrTrpValAspAsp 296
Qy 1847 -----GGGACAGGGGCTTCTACGACTGCAACCTCAACTGGGACTAAAATCGCTATATT 1900
Db 297 ThrAlaSerThrProLysThrLysThrAlaThrLeuAlaThrThrAsnThrGlyTyrLeu 316
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Db 912 TyrAsnIleAsnCysGlySerLysPheArgPhe 922

RESULT 7

US-09-198-452A-468

; Sequence 468, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1999-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 468

; LENGTH: 671

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-468

Alignment Scores:

| Pred. No.: | 3,92e-103 | Length: | 671 |
|------------------------|-----------|---------------|-----|
| Score: | 1264.00 | Matches: | 285 |
| Percent Similarity: | 62.43% | Conservative: | 132 |
| Best Local Similarity: | 42.66% | Mismatches: | 226 |
| Query Match: | 23.37% | Indels: | 25 |
| DB: | 4 | Gaps: | 15 |

US-09-428-122-1 (1-3000) x US-09-198-452A-468 (1-671)

| | | | |
|----|-----|---|-----|
| QY | 101 | ATGAAGTCTCTTTCCCAAGTTGTATTCTACATTGCTATTTTC---CCTTGTCT | 157 |
| Db | 1 | MetLysSerSerValSerTirPLeuPhePheSerSerIleProLeuPheSerSerLeuSer | 20 |
| QY | 158 | ATGATTGTACCGAGACAGTITTCGATTCAAGT---CGGAGTTTCGATGGATAAAAAAT | 214 |
| Db | 21 | IleValAlaAlaGluValThrLeuAspSerSerAsnAsnSerTyrAspGlySerAsnGly | 40 |
| QY | 215 | GGTAATTTTTCAGTTCGTCGAGAGTCAGGAA--GATGCTGGAACCTACCTACTATTTAAG | 271 |
| Db | 41 | ThrThrPheThrValPheSerThrThrAspAlaAlaAlaGlyThrThrTyrSerLeuLeu | 60 |
| QY | 272 | GGAAATGTCACTCTAGAAAAATATTCCTGGAAACAGGCACAGCAATCACAAAAAGCTGTTT | 331 |
| Db | 61 | SerAspValSerPheGlnAsnAlaGlyAlaLeuGlyIleProLeuAlaSerGlyCysPhe | 80 |
| QY | 332 | AACAACACTAAGGCGATTTCATTTTCACAGGTAAACGGAACTCTCTATTGTTCCAAACG | 391 |
| Db | 81 | LeuGluAlaGlyGlyAspLeuThrPheGlnGlyAsnGlnHisAlaLeuLysPheAlaPhe | 100 |
| QY | 392 | GTGGATGTCAGGACTGTAGCAGGGGCTGCTGTAAACAGCAGCGTGTAGATAAAATCTACC | 451 |
| Db | 101 | IleAsnAlaGlySerSerAlaGlyThrValAlaSerThrSerAlaAlaAspLysAsnLeu | 120 |
| QY | 452 | ACGTTTATAGGGTTTTTCTCGCTATCTTTTATTGCGTCTCCTGGAGTTCGATAACT--- | 508 |
| Db | 121 | LeuPheAsnAspPheSerArgLeuSerIleIleSerCysProSerLeuLeuSerPro | 140 |
| QY | 509 | ACCGCAAAAGGACCGTGTAGCTGCTCAGGGTAGCTTCAGTTTCGACAAAAAATGTCAGT | 568 |
| Db | 141 | ThrGlyGlnCysAlaLeuLys---SerValGlyAsnLeuSerLeuThrGlyAsnSerGln | 159 |
| QY | 569 | TTGCTCTTCAGCAAAAACCTTTCAACGGATAATGCGGTGCTATCACCGCAAAAACCTCT | 628 |
| Db | 160 | IleIlePheThrGlnAsnPheSerSerAspAsnGlyGlyValIleAsnThrLysAsnPhe | 179 |
| QY | 629 | TCATTAAACAGGACTACAAATGTTCAGTCTGTTTCTGAAAATAC---TCCTCAAAG | 682 |
| Db | 180 | LeuLeuSerGlyThrSerGlnPheAlaSerPheSerArgAsnGlnAlaPheThrGlyLys | 199 |
| QY | 683 | AAAGCGGAGCCATTTCAGACTTCCGATGCCCTTACCATTTACTGGAAACCAAGGGGAATC | 742 |

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QY 1805 TTCCATTACGGTATCAGGGAACCTGGGGCCCAATTTGTTGGGGACAGGGCCTTCTACG 1864
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
571 ThrHisTyrGlyTyrGlnGlyAsnTrp---GlnLeuSerTrpAlaAsnAlaThrSerSer 589
QY 1865 ---ACTGCACCTTCAACTGGAGTAAACTGGGTATATCTTAATCCCGAGCGTATCGGC 1921
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
590 LysIleGlySerIleAsnTrpThrArgThrGlyTyrIleProSerProGluArgLysSer 609
QY 1922 TCTTTAGTCCCTAATAGCTTATGGAATGCAATTTATAGATATTAGCTTCTCCATTAATCTT 1981
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
610 AsnLeuProLeuAsnSerLeuTrpGlyAsnPheIleAspIleArgSerIleAsnGlnLeu 629
QY 1982 ATGAGACTGCAAACGAAGGTTGCAGGAGACCGTCTTTTGGTGCTCGATTAATCT 2041
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
630 IleGluThrLysSerSerGlyGluProPheGluArgGlu-TyrGlyPheGlnGluLeuAr 649
QY 2042 AACTCTCTCCATAAGGATAGTA 2063
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
649 gileSerSerIleGluIleLeu 656

RESULT 8
US-09-198-452A-30
; Sequence 30, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 30
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-30

Alignment Scores:
Pred. No.: 6,26e-99 Length: 230
Score: 1214.00 Matches: 226
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 22.44% Indels: 0
DB: 4 Gaps: 0

US-09-428-122-1 (1-3000) x US-09-198-452A-30 (1-230)
QY 2204 CAAGGTACAGTCTACGGAGGAACCTCTCTATTACAGACACAGAAACCTATATCTCTTT 2263
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
4 LysGlyThrValTyrGlyGlyThrLeuTyrTyrGlnHisAsnGluThrTyrIleSerLeu 23
QY 2264 CCTTGCAAACTACGGCTCTGCTGCTGTATTGTTCTTACAGAGATTCCTGTTCTCTTT 2323
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
24 ProCysLysLeuArgProCysSerLeuSerTyrValProThrGluLeuProValLeuPhe 43
QY 2324 TCAGGAAACCTTAGCTACACCCATACGGATAACGATCGTGAACCAAGTATACAAATAT 2383
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
44 SerGlyAsnLeuSerTyrThrHisThrAspAsnAspLeuLysThrLysTyrThrThrTyr 63
QY 2384 CCTACTGTTAAAGAAAGCTGGGGAATGATAGTTTTCCTTTAGAAATTCGGTGAAGACT 2443
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
64 ProThrValLysGlySerTyrPgiYAsnAspSerPheAlaLeuGluPheGlyGlyArgAla 83
QY 2444 CCGATTGCTTAGTAAGTCTCTATTGAGCAGTACATGCCCTTCATGAATTTGCAG 2503
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 ProIleCysLeuAspGluSerAlaLeuPheGluGlnTyrMetProPheMetLysLeuGln 103
QY 2504 TTTGCTCTATGCATCAGGAAGGTTTAAAGAACAGGAAACAGAAAGCTCCGTGAATTTGGA 2563
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
104 PheValTyrAlaHisGlnGluGlyPheLysGluGlnGlyThrGluAlaArgGluPheGly 123
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QY 2564 AGTAGCCCTTGTGAATCTTCCCTTACCTATCGGATCCGATTTGATAGGAATCAGAC 2623
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
124 SerSerArgLeuValAsnLeuAlaLeuProIleGlyIleArgPheAspLysGluSerAsp 143
QY 2624 TGCCAAAGATCAACACGTACAACTTAACCTTGTGTATATCTGTGGATCTTGTTCGTAGTAAC 2683
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
144 CysGlnAspAlaThrTyrAsnLeuThrLeuGlyTyrThrValAspLeuValArgSerAsn 163
QY 2684 CCCGACTGTACGACAACTCGCAATTAGCGGTGATTTCTTGAAACACCTTCGGTACGAAT 2743
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
164 ProAspCysThrThrThrLeuArgIleSerGlyAspSerTrpLysThrPheGlyThrAsn 183
QY 2744 TTGGCAAGACAGCTTTAGTCTCTCGTCAGGAGACCACTTTTGTCTTAACCTCAAAATTT 2803
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
184 LeuAlaArgGlnAlaLeuValLeuArgAlaGlyAsnHisPheCysPheAsnSerAsnPhe 203
QY 2804 GAAGCCTTTAGCCAAATTTTCTTTGAATTTGGTGGGTCACTCTCGCAATTAACAATGTAGAC 2863
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
204 GluAlaPheSerGlnPheSerPheGluLeuArgGlySerSerArgAsnTyrAsnValAsp 223
QY 2864 TTAGAGCAAAATACCAATTC 2884
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
224 LeuGlyAlaLysTyrGlnPhe 230

RESULT 9
US-09-198-452A-32
; Sequence 32, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 32
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-32

Alignment Scores:
Pred. No.: 6,85e-98 Length: 507
Score: 1204.00 Matches: 241
Percent Similarity: 62.88% Conservative: 86
Best Local Similarity: 46.35% Mismatches: 168
Query Match: 22.26% Indels: 25
DB: 4 Gaps: 9

US-09-428-122-1 (1-3000) x US-09-198-452A-32 (1-507)
QY 1360 CTTTCACAGG-----AGAAAAGTTATCAGACACAGAGCGCGAGATTCTAAAAATCT 1410
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2 LeuHisArgPheLeuTrpArgGluThrLeuArg-SerLysLysProAsp-----AsnLeu 19
QY 1411 TACTTCGAAGCTACTACAGCCTGTAACTCTTTTCAGGAGGTACTCTATCTTTAAAAACATCG 1470
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
19 uLysSerThrPheThrGlnAlaValGluLeuAlaGlyAlaLeuValLeuLysAspG1 39
QY 1471 AGTGACTCTGCAGACTCAGGCATTCTCAACAGGAGGATTTCTGCTCGAATTCGACGT 1530
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
39 yValThrValValAlaAsnThrIleThrGlnValGluGlySerLysValValMetAspG1 59
QY 1531 AGGAATCTACTAGAA---CCTGCTGATACTAGCACCATTAACAATTTCTGTCATTAAACAT 1587
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
59 yGlyThrThrPheGluAlaSerAlaGlyValThrLeuAsnGlyLeuAlaIleAsn11 79
QY 1588 CAGTTCTATAGACGGTGCAGAAAGGCAAAATAGAAACCAAGCTACGTCAAAAATCT 1647
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
79 eAspSerLeuAspGlyThrAsnLysAlaIleIleLysAlaThrAlaAlaSerLysAspVa 99
```



```
QY 1648 GACATTTATCTGGAACCATCTATTATTTGGACCCGACGGCAGCTTTTATGAAATCATAG 1707
Db : ||||| ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
99 lAlaLeuSerGlyProIleMetLeuValAspAlaGlnGlyAsnTyrTyrGluHisHisAs 119
QY 1708 TTTTAAAGAAATCCTCAGTCCCTACGACATCTTAGACTCAAAAGCTTCTCGAACTGTAAACAAG 1767
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
119 nLeuSerGlnGlnValPheAlaLeuIleGluLeuSerAlaGlnGlyThrMetThrTh 139
QY 1768 CACGCGCAGTACTCCAGATCCCTATATGAGTGTAGAAATTCCTACCGCTATCAGGAAC 1827
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
139 rThraspileProAspThrProIleLeuAsnThrThrAsnHisTyrGlyIleLysGlyTh 159
QY 1828 TTGGGGCCCAATGTTGG-----GGACAGGGGCTTCTACGACTGCACACCTTCAA 1878
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
159 r---GlyIleIleValTrpValAspAlaThrAlaLysThrLysAsnAlaThrLeuTh 178
QY 1879 CTGGACTAAACTGGCTATATTCCTAAATCCGAGCTATCGGCTCTTTAGTCCCTAATAG 1938
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
178 rTrpThrLysThrGlyTyrLysProAsnProGluArgGlnGlyProLeuValProAsnSe 198
QY 1939 CTTATGGAATCATTTATAGTCTCTCTCCATTAATCTTATGGAGACTGCACAAAGA 1998
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
198 rLeuTrpGlySerPheValAspValArgSerIleGlnSerLeuMetAspArgSerThrSe 218
QY 1999 AGGGTTGAGGAGACCGTCTTTTGGTGTGCTGATTATCTAACTTCTTCCATAGGA 2058
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
218 rSerLeuSerSerThrAsnLeuTrpValSerGlyIleAlaAspPheLeuHisGluAs 238
QY 2059 TAGTCAAAAACACACACGCGGTTTCGCCATTTAGTGGCGGTTATGTCAATAGGAGGAAA 2118
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
238 pGlnLysGlyAsnGlnAArgSerTyrArgHisSerSerAlaGlyTyrAlaLeuGlyGlyG 258
QY 2119 CCTACATATCTGTCAGATAAGATCTTAGTGCTCTCATTTTGTCTAGCTCTTTGGAGAGA 2178
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
258 yPhePheThrAlaSerGluAsnPhePheAsnPheAlaPheCysGlnLeuPheGlyTyrAs 278
QY 2179 TAGACACTACTTTGAGCTAAGAACTCAAGGTACACTACGGAGGAACCTCTATTACCA 2238
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
278 pLysAspHisLeuValAlaLysAsnHisThrHisValTyrAlaGlyAlaMetSerTyrAr 298
QY 2239 GCAC-----AACGAAACCTATATCTCTCTCTGCAAACTACGGCCTTGTGCTT 2289
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
298 gHisLeuGlyGluSerLysThrLeuAlaLysIle-----Le 310
QY 2290 GTCTATGTTCTCAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCTACACCCATAC 2349
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
310 uSerGlyAsnSerAspSerLeuPheValPheAsnAlaArgPheAlaTyrGlyHisTh 330
QY 2350 GGATACGATCTGAAACCAAGTATACACATATCTACTGTTTAAAGGAAGCTGGGGAA 2409
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
330 rAspAsnAsnMetThrThrLysTyrThrGlyTyrSerProValLysGlySerTrpGlyAs 350
QY 2410 TGATAGTTTCGGCTTTAGAAATTCGGTGAAGAGCTCCGATTTCGTTAGAT---GAAAGTGC 2466
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
350 nAspAlaPheGlyIleGluCysGlyAlaIleProValValAlaSerGlyArgArgSe 370
QY 2467 TCTATTTAGCAGCTACATGCCCTTCTAGAAATTCAGTTGTCTATGCACTCAGGAAGG 2526
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
370 rTrpValAspThrHisThrProPheLeuAsnLeuGluMetIleTyrAlaHisGlnAsnAs 390
QY 2527 TTTTAAAGACAGGACAGAGCTCGTGAATTTGGAGTAGCCGCTTGTGAATCTTCG 2586
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
390 pPheLysGluAsnGlyThrGluGlyArgSerPheGlnSerGluAspLeuPheAsnLeuAl 410
QY 2587 CTTTACCTATCGGATCCGATTTTGATAAGGAATCAGACTGCGCAAGATGCAACGTACAATCT 2646
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
410 aValProValGlyIleLysPheGluLysPheSerAsp-----LysSerThrTyrAspLe 428
QY 2647 AACTCTTGTTATCTAGTGTGATCTTGTTCGTAGTAAACCCGAGCTAGCAGCAACATCGG 2706
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
428 uSerIleAlaTyrValProAspValIleArgAsnAspProGlyCysThrThrThrLeuMe 448
```

```
QY 2707 AATTAGCGGTGATTCTTGGAAAACCTTCGTGTACGAATTTGGCAAGACAGCTTTAGTCCT 2766
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
448 tValSerGlyAspSerTrpSerThrCysGlyThrSerLeuSerArgGlnAlaLeuLeuVa 468
QY 2767 TCTGTCAGGAAACCATTTTGTCTTTAACTCAATTTTGAAGCCTTTAGCCAAATTTCTTT 2826
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
468 lArgAlaGlyAsnHisHisAlaPheAlaSerAsnPheGluValPheSerGlnPheGluVa 488
QY 2827 TGAATTTGCGTGGCTCATCTCGCAATTAACAATGTAGACTTAGGAGCAAAATACCAATTC 2884
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
488 lGluLeuArgGlySerSerArgSerTyrAlaIleAspLeuGlyGlyArgPheGlyPhe 507

RESULT 10
US-09-198-452A-466
; Sequence 466, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 466
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-466

Alignment Scores:
Pred. No.: 3,38e-91 Length: 1132
Score: 1130.00 Matches: 316
Percent Similarity: 39.28% Conservative: 133
Best Local Similarity: 27.55% Mismatches: 310
Query Match: 20.89% Indels: 384
DB: 4 Gaps: 24

US-09-428-122-1 (1-3000) x US-09-198-452A-466 (1-1132)
QY 101 ATGAAGTCTTCTTTCCCAAGTTTGTATTTTCTACATTTGCTATTTTCCCTTTG---TCT 157
Db 1 MetLysTyrSerLeuProTrpLeuThrSerSerAlaLeuValPheSerLeuHisPro 20
QY 158 ATGATTGCTACCGACAGAGTTTGTGATTCAAGTCGAGTTTCGATGGGAATAAAATCGT 217
Db 21 LeuMetAlaAlaAsnThrAspLeuSerSerSerAspAsnTyrGluAsnGlySerSerGly 40
QY 218 AAT-----TTTTCAGTTTCGTGAGAGTCAGGAAGATGCTGGAACCTACTACTATTTAAG 271
Db 41 SerAlaAlaPheThrAlaLysGluThrSerAspAlaSerGlyThrTyrThrLeuThr 60
QY 272 GGAATGTCACTCTAGAAAAATATTCCTGGACAGCAGCAGCAATCACA-----AAA 322
Db 61 SerAspValSerIleThrAsnVal-----SerAlaIleThrProAlaAspLys 76
QY 323 AGCTCTTTTAAACACACACTAAGCGGATTTGATTTTCACAGGTACAGGGAACCTCTTATG 382
Db 77 SerCysPheThrAsnThrGlyGlyAlaLeuSerPheValGlyAlaAspHisSerLeuVal 96
QY 383 TTCCAACAGGTGGATGTCAGGAGCTGTAGCAGGGGCTGTGTAAACAGCAGCGTGTAGAT 442
Db 97 LeuGlnThrIle---AlaLeuThrHisAspGlyAlaAlaIleAsnAsnThr-----Asn 113
QY 443 AAATCTACACGTTTATAGGGTTTCTTCGCTATCTTTTATTCGCTCTCTCGGAAGTTGCG 502
Db 114 ThrAlaLeuSerPheSerGlyPheSerSerLeuLeuIleAspSerAlaProAlaThrGly 133
QY 503 ATAACCTACCGCAAGAGCCCTTAGCTGCTCTAGC-----GGTAGCTTGAGT 550
Db 134 ThrSerGlyGlyLeGlyAlaIle---CysValThrAsnThrGluGlyGlyThrAlaIthr 152
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866 AsLeuLysPheHisAsnAsnGluGlySerPheTyrAspAsnProGlyLeuLysAlaAsn 885
1721 CAGTCTACGACATCTTAGAGCTCAAAGCT---TCTGGAACTGTAAACACCGCAGTG 1777
886 LeuAsnLeuProPheLeuAspLeuSerSerThrGlyThrValAsnLeuAspPhe 905
1778 ACTCCAGATCTTAATAGGTGGTGAAGAAATTCATTACCGCTATCGGAACTTGGGC--- 1834
906 AsnProIleProSerSerMetAlaAlaProAspTyrGlyTyrGlnGlySerThrLeu 925
1835 ---CCAATTGTTTGGGACAGGGCTTCTACGACTCAACCTTCAACTGACTGCTAAACT 1891
926 ValProLysVal---GlyAlaGlyGlyLysValThrLeuValAlaGluTrpGlnAlaLeu 944
1892 GGCCTATATCTTAATCCCGACGCTATCGCTCTTTAGTCCCTAATAGCTTTATGAATGCA 1951
945 GlyTyrThrProLysProGluLeuArgAlaThrLeuValProAsnSerLeuTrpAsnAla 964
1952 TTTATAGATATAGCTCTCTCCATTATCTTAGGAGACTGCAACGAGGGTTGCAGGA 2011
965 TyrValAsnIleHisSerIleGlnGlnGluIleAlaThrAlaMetSerAspAlaProSer 984
2012 GACCGTCTTTTGGTGGCTGATTAATCTACTTCTCCATAAGGATAGTACAAACA 2071
985 HisProGlyIleTrpIleGlyGlyIleGlyAsnAlaPheHisGlnAspLysGlnLysGlu 1004
2072 CGACCGGTTTTCGCATTTAGTGGCGTTATGTATCATAGGAAACCTACATCTGT 2131
1005 AsnAlaGlyPheArgLeuIleSerArgGlyTyrIleValGlyGlySerMetThrThrPro 1024
2132 TCAGATAAGATCTTTAGTGTGCATTTGTGCTCTTGTGAGAGATAGACTACTTT 2191
1025 GlnGluTyrThrPheAlaValAlaPheSerGlnLeuPheGlyLysSerLysAspTyrVal 1044
2192 GTAGTGAAGATCAAGGTACAGTACGAGGAACTCTCTATACAGCAACCAAC 2251
1045 ValSerAspIleLysSerGlnValTyrAlaGlySerLeuCysAlaGln---SerSerTyr 1063
2252 TATATCTCTCTCTCCATTGCAAACTAGCGCTTCTCGTTGCTTATGTT----- 2299
1064 ValIleProLeuHisSerSerLeuArgArgHisValLeuSerLysValLeuProGluLeu 1083
2300 CCTACAGAGATCTCTGTTCTCTTTTTCAGAAACCTTAGTACACCCATCAGGATACGAT 2359
1084 ProGlyGluThrProLeuValLeuHisGlyGlnValSerTyrGlyArgAsnHisAsn 1103
2360 CTGAAACCAAGTATACACATATCTACTGTTAAAGGAAGCTGGGGGAATGATGTTTC 2419
1104 MetThrThrLysLeuAlaAsnAsnThrGlnGlyLysSerAspTrpAspSerHisSer 1123
2420 GCTTTAGAA 2428
1124 LeuLeuLys 1126

RESULT 11
US-09-556-877-190
; Sequence 190, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 190
; LENGTH: 1006

TYPE: PRT
ORGANISM: Chlamydia
US-09-556-877-190
Alignment Scores: 6.53e-91 Length: 1006
Pred. No.: 1126.50 Matches: 303
Score: 46.02% Conservative: 160
Best Local Similarity: 30.12% Mismatches: 372
Query Match: 20.83% Indels: 171
DB: 4 Gaps: 30
US-09-428-122-1 (1-3000) x US-09-556-877-190 (1-1006)
QY 242 GAGATGCTGGAACTACCTATTAAGGAAATGTCTACTAGAAAATATTCCTCGGA 301
Db 47 AspProSerGlyThrValPheSerAlaGlyGluLeuThrLeuLysAsnLeuAspAsn 66
QY 302 ACAGGCACAGCAATCAAAAAGCTGTTTAAACAACACTAAGGGCGATTTCCTTCA 361
Db 67 SerIleAlaAlaLeuProLeuSerCysPheGlyAsnLeuLeuGlySerPheThrValLeu 86
QY 362 GGTAAACGGGAATCTCTATTGTTCCAAACCGTGGATGCAGGACTGTAGCAGGGCTGCT 421
Db 87 GlyArgGlyHisSerLeuThrPheGluAsnIleArgThrSerThr---AsnGlyAlaAla 105
QY 422 GTTAAACAGCAGCTGTAGATAAATCTACCAACGTTTATAGGTTTCTTCGCTATCTTT 481
Db 106 LeuSerAsnSerAlaAlaAspGlyLeuPheThrIleGluGlyPheLysGluLeuSerPhe 125
QY 482 ---ATTGCTCTCTCTGGAAAGTTTCGATACTACCGCAAGAGCGCGTT 526
Db 126 SerAsnCysAsnSerLeuLeuAlaValLeuProAlaAlaThrThrAsnLysGlySerGln 145
QY 527 AGCTGCTCTACGGTAGC-----TTGAGT 550
Db 146 ThrProThrThrThrSerThrProSerAsnGlyThrIleTyrSerLysThrAspLeuLeu 165
QY 551 TTGACAAAATATGTCAGTTTCTCTCAGCAAAAACCTTTCAACGGATAATGGCGGTGCT 610
Db 166 LeuLeuAsnAsnGluLysPheSerPheTyrSerAsnLeuValSerGlyAspGlyGlyAla 185
QY 611 ATCACCAGCAAAACTCTTTCAATTAACAGGGACTCAATGTCAGCTCTGTTTCTGAAAT 670
Db 186 IleAspAlaLysSerLeuThrValGlnGlyIleSerLysLeuCysValPheGlnGluAsn 205
QY 671 ACCTCCTCAAAAGAGGGAGGCCATTACAGCTCCGATGCCCTTACCATTACTGGAAC 730
Db 206 ThrAlaGlnAlaAspGlyGlyAlaCysGlnValValThrSerPheSerAlaMetAlaAsn 225
QY 731 CAAGGGGAAGTCTCTTTT----- 748
Db 226 GluAlaProIleAlaPheValAlaAsnValAlaGlyValArgGlyGlyIleAlaAla 245
QY 749 -----TCTGCAATATCTTCTCGGATCT----- 772
Db 246 ValGlnAspGlyGlnGlnGlyValSerSerThrThrThrGluAspProValValSer 265
QY 773 -----GGAGCTGCAATT 784
Db 266 PheSerArgAsnThrAlaValGluPheAspGlyAsnValAlaArgValGlyGlyIle 285
QY 785 TTTCAGAGAGCTCGTGTGACTATTTCTAATATGATAAGTTTCTTTTATGACAAAT--- 841
Db 286 TyrSerTyrGlyAsnValAlaPheLeuAsnAsnGlyLysThrLeuPheLeuAsnVal 305
QY 842 -----AAGGTCACAGGAGCGGACTCTTCAACACG 871
Db 306 AlaSerProValTyrIleAlaAlaLysGlnProThrSerGlyGlnAlaSerAsnThrSer 325
QY 872 GGGGATATG---TCAGGAGGTGCTATCTCTGCTGTATAA-----ACTACT 913
Db 326 AsnAsnTyrGlyAspGlyAlaIlePheCysLysAsnGlyAlaGlnAlaGlySerAsn 345

QY 914 ACAGATACTAAGGTCCACCTCACTGGAAATCAGATGTTACTCTTCACGAACAATACATCG 973
Db : : : : :
QY 346 AsnSerGlySerValSerPheAspGlyGluGlyValPhePheSerSerAsnValala 365
: : : : :
QY 974 ACAACAGCGGAGGAGTATCTATGTGCAAAAAGTCGAACCTGGCTCCGAGGACTTACC 1033
Db : : : : :
QY 366 AlaGlyLysGlyAlaIleTyrAlaLysLysLeuSerValalaAsnCysGlyProVal 385
: : : : :
QY 1034 CTATTCAGTGAATAGTGTCATCAATGAGGTACAGCTCCTAAAGTGGAGCATAGCTATC 1093
Db : : : : :
QY 386 GlnPheLeuArgAsnIleAlaAsn- - - - -AspGlyGlyAlaIleTyrLeu 400
: : : : :
QY 1094 GAACATAGTGGGAATGAGTTTATCCCGCATAGTAGTGGTCACATGCTCTTTTAGGGAAT 1153
Db : : : : :
QY 401 GlyGluSerGlyGluLeuSerLeuSerAlaAspTyrGlyAspIleIlePheAspGlyAsn 420
: : : : :
QY 1154 - - - - -ACAGTCACTTCTACTACTCTCGGACGAAT - - - - -AGAAGT 1189
Db : : : : :
QY 421 LeuLysArgThrAlaLysGluAsnAlaAspValasnGlyValThrValSerSerGln 440
: : : : :
QY 1190 AGTATCGACTTAGAAGCAGGTGCAAGATGACAGCTTTGGCTTCTGCTGCTGGTAGAGCC 1249
Db : : : : :
QY 441 AlaIleSerMetGlySerGlyGlyLysIleThrThrLeuArgAlaLysAlaGlyHisGln 460
: : : : :
QY 1250 ATCTACTTCTATGCCATAACTACAGGATCATCCACA - - - - -GTTACA 1297
Db : : : : :
QY 461 IleLeuPheAsnAspProIleGluMetAlaAsnGlyAsnGlnProAlaGlnSerSer 480
: : : : :
QY 1298 GATGCTTAAAGTAAATAGACATCCCGCAGATTCTGCACATATACAGGGAACATC 1357
Db : : : : :
QY 481 LysLeuLysIleAsnAspGlyGluGly - - - - -TyrThrGlyAspIle 495
: : : : :
QY 1358 ATCTTCACAGAGAAAAGTTATCAGACAGAGCCGACAGATTCCTAAATCTTACTTCG 1417
Db : : : : :
QY 496 ValPheAla - - - - -AsnGlySerSer 502
: : : : :
QY 1418 AAGCTACTACAGCCTGTAACCTCTTTCAGGAGTACTCTATCTTTAAACATCGAGTACT 1477
Db : : : : :
QY 503 ThrLeuTyrGlnAsnValThrIleGluGlnGlyArgIleValLeuArgGluLysAlaLys 522
: : : : :
QY 1478 CTGCAGACTCAGGCATTCACATCAACAGGCAGATTCCTGCTCGAAATGGAGTAGGAAC 1537
Db : : : : :
QY 523 LeuSerValAsnSerLeuSerGlnThrGlySer - - - - -LeuTyrMetGluAlaGlySer 541
: : : : :
QY 1538 ACTCTAGAA - - - - -CTGCTGATACTAGC - - - - - 1561
: : : : :
QY 542 ThrLeuAspPheValThrProGlnProGlnProAlaAlaAsnGlnLeuIle 561
: : : : :
QY 1562 ACCATAACAATTTGGTCATTAAACATCAGTTCTATA - - - - - 1597
: : : : :
QY 562 ThrLeuSerAsnLeuHisLeuSerLeuSerSerLeuLeuAlaAsnAlaValThrAsn 581
: : : : :
QY 1598 - - - - -GACGGTGCAAAGAGGCAAAAATAGAAACCAAGCTACG 1636
Db : : : : :
QY 582 ProProThrAsnProProAlaGlnAspSerHisProAlaValIleGlySer - - - - -ThrThr 600
: : : : :
QY 1637 TCAAAAATCTGACTTTATCTGAAACCATCATCTTATTTGACCCGAGCGGCATTTTAT 1696
Db : : : : :
QY 601 AlaGlySerValThrIleSerGlyProIlePhePheGluAspLeuAspAspThrAlaTyr 620
: : : : :
QY 1697 GAAATCATAGT - - - - -TAAAGAAATCCTGACCTCCTACGACATCTTAGAGCTCAAGCTTCT 1753
Db : : : : :
QY 621 AspArgTyrAspTrpLeuGlySerAsnGlnLysIleAsnValLeuLysLeuGlnLeu - - - - - 639
: : : : :
QY 1754 GGAACTGTAAACAGACCGCAGTGCATCCAGATCCTATAATGGGTGAGAAATTC - - - - -CAT 1810
Db : : : : :
QY 640 GlyThrLysProProAlaAsnAlaProSerAspLeuThrLeuGlyAsnGluMetProLys 659
: : : : :
QY 1811 TACGGCTATCAGGGAACTTGGGGCCCAATTTGTTGGGGGACAGGGGCTTCTACGACTGCA 1870
Db : : : : :
QY 660 TyrGlyTyrGlnGlySerTrp - - - - -LysLeuAlaTrpAspProAsnThrAlaAsnAsnGly 678
: : : : :

QY 1871 ACCTTC - - - - -AACTGCACTAAACGGCTATATTCTCTAATCCGAGCGTATC 1918
Db : : : : :
QY 679 ProTyrThrLeuLysAlaThrTrpThrLysThrGlyTyrAsnProGlyProGluArgVal 698
: : : : :
QY 1919 GGCCTTTAGTCCTTAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCTCCATTAT 1978
Db : : : : :
QY 699 AlaSerLeuValProAsnSerLeuTrpGlySerIleLeuAspIleArgSerAlaHisSer 718
: : : : :
QY 1979 CTTATGAGACTGCCAACGAAGGGTTCGAGGGAGACCGTCTTTTGGTGTGCTGGAA 2038
Db : : : : :
QY 719 AlaIleGlnAlaSerValAspGlyArgSerTyrCysArgGlyLeuTrpValSerGlyVal 738
: : : : :
QY 2039 TCTAACTTCTTCATAGGATAGTACAAAACACGACGCGGTTTCGCCATTTGAGTGCC 2098
Db : : : : :
QY 739 SerAsnPhePheTyrHisAspArgAspAlaLeuGlyGlnGlyTyrArgTyrIleSerGly 758
: : : : :
QY 2099 GGTATGTCTATAGAGGAACCTACATCTTGTTCAGATAAGATTTCTTAGTGTGCTGCA 2158
Db : : : : :
QY 759 GlyTyrSerLeuGlyAlaAsnSerTyrPheGlySer - - - - -SerMetPheGlyLeuAlaPhe 777
: : : : :
QY 2159 TGTACGCTCTTTCGAGAGATAGAGACTACTTTGTAGCTAAGAAATCAAGTACAGTCTAC 2218
Db : : : : :
QY 778 ThrGluValPheGlyArgSerLysAspTyrValValCysArgSerAsnHisAlaCys 797
: : : : :
QY 2219 GGAGGAACCTCTATTACACGACACAAACCACTATATCTCTCTCTTCCAACTACGG 2278
Db : : : : :
QY 798 IleGlySerValTyrLeuSerThrGlnGlnAlaLeu - - - - - 809
: : : : :
QY 2279 CTTTGTGCTGTCTTATGTTCTTACAGAGATTCTCTGTTCTCTTTTCAGGA - - - - - 2329
Db : : : : :
QY 810 - - - - -CysGly - - - - -SerTyr - - - - -LeuPheGlyAspAlaPheIle 820
: : : : :
QY 2330 AACCTTAGCTACACCCATACGATACGATCTGAAACCAAGTATACAAATATCTTACT 2389
Db : : : : :
QY 821 ArgAlaSerTyrGlyPheGlyAsnGlnHisMetLysThrSerTyrThrPheAlaGluGlu 840
: : : : :
QY 2390 GTTAAAGGAGCTGGGGGAATGATGTTTCGCTTTAGATTTCGGTGAAGAGCTCCGATT 2449
Db : : : : :
QY 841 SerAspValArgTrpAspAsnAsnCysLeuAlaGlyGluIleGlyAlaGlyLeuProIle 860
: : : : :
QY 2450 TGTCTAGATGAAATGCTCTTATTT - - - - -GAGCAGTACATGCCCTTCATGAAATTCAGTTT 2506
Db : : : : :
QY 861 ValIleThrProSerLysLeuTyrLeuAsnGluLeuArgProPheValGlnAlaGluPhe 880
: : : : :
QY 2507 GTCTATGCATCAGGAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGT 2566
Db : : : : :
QY 881 SerTyrAlaAspHisGluSerPheThrGluGluGlyAspGlnAlaArgAlaPheLysSer 900
: : : : :
QY 2567 AGCGCTCTTGTAATCTTGCTTACCTATCGGATCGGATTCGATTAAGGAATCAGACTGC 2626
Db : : : : :
QY 901 GlyHisLeuLeuAsnLeuSerValProValGlyValLysPheAspArgCysSerSerThr 920
: : : : :
QY 2627 CAAGATGCAACGTACAACTCTTGTGTATCTGTGTGATCTGTCTGTAGTAAACCC 2686
Db : : : : :
QY 921 HisProAsnLysTyrSerPheMetAlaAlaTyrIleCysAspAlaTyrArgThrIleSer 940
: : : : :
QY 2687 GACTGTACGACACACTCGGAATAGCGGTGATCTTGGAAAACCTTCGGTACGAATTTG 2746
Db : : : : :
QY 941 GlyThrGluThrThrLeuLeuSerHisGlnGluThrTriphThrThrAspAlaPheHisLeu 960
: : : : :
QY 2747 GCAAGCAAGCTTTAGCTCTCTCGTCGAGGGAACCATTTTGTCTTAACTCAATTTTGA 2806
Db : : : : :
QY 961 AlaArgHisGlyValValValArgGlySerMetTyrAlaSerLeuThrSerAsnIleGlu 980
: : : : :
QY 2807 GCCTTTAGCCAAATTTCTTTTGAATTTGCGTGGGTCACTCGCAATTTACAGTACTTA 2866
Db : : : : :
QY 981 ValTyrGlyHisGlyArgTyrGluTyrArgAspAlaSerArgGlyTyrGlyLeuSerAla 1000
: : : : :
QY 2867 GGAGCAAAATACCAATTC 2884
Db : : : : :
QY 1001 GlySerLysValArgPhe 1006
: : : : :

US-09-620-412C-190
; Sequence 190, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620.412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: PastSeq for Windows Version 3.0/4.0
; SEQ ID NO 190
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-620-412C-190

Alignment Scores:
Pred. No.: 6,53e-91 Length: 1006
Score: 1126.50 Matches: 303
Percent Similarity: 46.02% Conservative: 160
Best Local Similarity: 30.12% Mismatches: 372
Query Match: 20.83% Indels: 171
Dbs: 4 Gaps: 30

US-09-428-122-1 (1-3000) x US-09-620-412C-190 (1-1006)

| | | | |
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| QY | 242 | GAAGATGCTGGAACTACCTACCTATTAAAGGAAATGTCACTCTAGAAAATATTCTCTGGA | 301 |
| Db | 47 | AspProSerGlyThrValPheSerAlaGlyGluLeuThrLeuLysAsnLeuAspAsn | 66 |
| QY | 302 | ACAGGCACAGCAATCAAAAAGCTGTTTAAACAACACTAAGGGCATTTGACTTTTACA | 361 |
| Db | 67 | SerIleAlaLeuProLeuSerCysPheGlyAsnLeuLeuGlySerPheThrValLeu | 86 |
| QY | 362 | GTAACGGAACTCTCTATTGTTCCAAACGGTGGATGACGGGACTGTACAGGGCTGCT | 421 |
| Db | 87 | GlyArgGlyHisSerLeuThrPheGluAsnIleArgThrSerThr---AsnGlyAlaAla | 105 |
| QY | 422 | GTTAACAGCAGCGTGTAGATAAATCTACAGCTTTATAGGGTTTCTTCGTATCTTTT | 481 |
| Db | 106 | LeuSerAsnSerAlaAlaAspGlyLeuPheThrIleGluGlyPheLysGluLeuSerPhe | 125 |
| QY | 482 | -----ATTGCGTCTCTCGAAGTTTCGATAACTACCGCAAGAGCCGTT | 526 |
| Db | 126 | SerAsnCysAsnSerLeuLeuAlaValLeuProAlaAlaThrThrAsnLysGlySerGln | 145 |
| QY | 527 | AGCTGCTCTACGGTAGC-----TTGAGT | 550 |
| Db | 146 | ThrProThrThrThrSerThrProSerAsnGlyThrIleTyrSerLysThrAspLeuLeu | 165 |
| QY | 551 | TTGACAAAAAATGTCAGTTTGCTCTTTCAGCAAAAATTTTTCACAGGATAATGGCGTGT | 610 |
| Db | 166 | LeuLeuAsnAsnGluLysPheSerPheTyrSerAsnLeuValSerGlyAspGlyAla | 185 |
| QY | 611 | ATCACCAGAAAACCTCTTCATTAAACAGGACTACAAATGTACGCTCTGTTTCTGAAAT | 670 |
| Db | 186 | IleAspAlaLysSerLeuThrValGlnGlyIleSerLysLeuCysValPheGlnGluAsn | 205 |
| QY | 671 | ACCTCTCAAAGAAAGCGGCGCATTCAGACTTCGATCCGCTTACCATTACTGGAAC | 730 |
| Db | 206 | ThrAlaGlnAlaAspGlyGlyAlaCysGlnValThrSerPheSerAlaMetAlaAsn | 225 |
| QY | 731 | CAAGGGGAAGTCTCTTT----- | 748 |
| Db | 226 | GluAlaProIleAlaPheValAlaAsnValAlaGlyValArgGlyGlyIleAlaAla | 245 |
| QY | 749 | -----TCTGCAAACTCTTCGGATCT----- | 772 |
| Db | 246 | ValGlnAspGlyGlnGlnGlyValSerSerThrSerThrGluAspProValValSer | 265 |
| QY | 773 | -----GGAGCTGCAATT | 784 |

| | | | |
|----|------|--|------|
| Db | 266 | PheSerArgAsnThrAlaValGluPheAspGlyAsnValAlaAlaArgValGlyGlyIle | 285 |
| QY | 785 | TTTACAGAAAGCCTGGTGAAGTATTCTTAATAAGTCTAAAGTTTCTTTATTGACAAT--- | 841 |
| Db | 286 | TyrSerTyrGlyAsnValAlaPheLeuAsnAsnGlyLysThrLeuPheLeuAsnAsnVal | 305 |
| QY | 842 | -----AAGTTCACAGGAGCGACTCTCAACACG | 871 |
| Db | 306 | AlaSerProValTyrIleAlaAlaLysGlnProThrSerGlyGlnAlaSerAsnThrSer | 325 |
| QY | 872 | GGGATATG---TCAGGAGGTGCTATCTGCTTATAAA-----ACTAGT | 913 |
| Db | 326 | AsnAsnTyrGlyAspGlyGlyAlaIlePheCysLysAsnGlyAlaGlnAlaGlySerAsn | 345 |
| QY | 914 | ACAGATACTAAGTCAACCTCAGTGAATACAGATGTTACTCTTCAGACAACATACATCG | 973 |
| Db | 346 | AsnSerGlySerValSerPheAspGlyGluGlyValPhePheSerSerAsnValAla | 365 |
| QY | 974 | ACAACAGGGGAGGAGCTATCTATGTGAAAAGCTCGAACTGGCTCCGGAGGACTTACC | 1033 |
| Db | 366 | AlaGlyLysGlyGlyAlaIleTyrAlaLysLysLeuSerValAlaAsnCysGlyProVal | 385 |
| QY | 1034 | CTATTTCAGTAGAAATAGTGTCAATGAGGTACAGCTCTCTAAAGGTGGAGCCATAGTATC | 1093 |
| Db | 386 | GlnPheLeuArgAsnIleAlaAsn-----AspGlyGlyAlaIleTyrLeu | 400 |
| QY | 1094 | GAAAGATGCGGGAATTAGTATTATCCGCCATAGTGTGATGTCATTGTTTGGGAAT | 1153 |
| Db | 401 | GlyGluSerGlyGluLeuSerLeuSerAlaAspTyrGlyAspIleIlePheAspGlyAsn | 420 |
| QY | 1154 | -----ACAGTCACCTTCTACTACTCTCTGGGAGCAAT-----AGAGT | 1189 |
| Db | 421 | LeuLysArgThrAlaLysGluAsnAlaAlaAspValAsnGlyValThrValSerSerGln | 440 |
| QY | 1190 | AGTATCGACTTAGCAACGAGTGCAAGATGACAGCTTTTGGCTTCTGCTGGTAGAGCC | 1249 |
| Db | 441 | AlaIleSerMetGlySerGlyGlyLysIleThrLeuArgAlaLysAlaGlyHisGln | 460 |
| QY | 1250 | ATCTACTTCTATGATCCCATTAACCTACAGGATCATCCACAACA-----GTACA | 1297 |
| Db | 461 | IleLeuPheAsnAspProIleGluMetAlaAsnGlyAsnAsnGlnProAlaGlnSerSer | 480 |
| QY | 1298 | GATGCTTTAAAGTTAATGAGACTCCGGCAGATTCTGCATCAATATACAGGGAACATC | 1357 |
| Db | 481 | LysLeuLeuLysIleAsnAspGlyGluGly-----TyrThrGlyAspIle | 495 |
| QY | 1358 | ATCTTTCACAGGAGAAAAGTTATACAGAGCAGAGCGCCAGAGTCTTAAAAATCTTACTCG | 1417 |
| Db | 496 | ValPheAla-----AsnGlySerSer | 502 |
| QY | 1418 | AGCTACTACAGCTGTAACTCTTTCAGAGGTACTCTATCTTTAAACATGGAGTGACT | 1477 |
| Db | 503 | ThrLeuTyrGlnAsnValThrIleGluGlnArgIleValLeuArgGluLysAlaLys | 522 |
| QY | 1478 | CTGCAGACTCAGGCAATTCACCAAGCAGAGATTCTCGTCTCGAAATCGACAGTGAAGT | 1537 |
| Db | 523 | LeuSerValAsnSerLeuSerGlnThrGlyGlySer---LeuTyrMetGluAlaGlySer | 541 |
| QY | 1538 | ACTCTAGAA-----CCTGCTGATACTAGC----- | 1561 |
| Db | 542 | ThrLeuAspPheValThrProGlnProGlnGlnProProAlaAlaAsnGlnLeuIle | 561 |
| QY | 1562 | ACATAAAACAATTTGGTCAATTAACATGACTTCTATA----- | 1597 |
| Db | 562 | ThrLeuSerAsnLeuHisLeuSerLeuSerLeuLeuAlaAsnAsnAlaValThrAsn | 581 |
| QY | 1598 | -----GACGCTGCAAGAGAGGCAAAAATAGAAACCAAGAGTACG | 1636 |
| Db | 582 | ProProThrAsnProProAlaGlnAspSerHisProAlaValIleGlySer---ThrThr | 600 |
| QY | 1637 | TCAAAAATCTGACTTTTATCTGGAAACCATCACTTTTATGGACCGCAGCGGACGTTTAT | 1696 |

Db 186 IleAspAlaLysSerLeuThrValGlnGlyIleSerLysLeuCysValPheGlnGluAsn 205
QY 671 ACCTCCTCAAGAAAGCGGAGCCATTGAGATCTCCGATGCCCTTACTGGAAC 730
Db 206 ThrAlaGlnAlaAspGlyGlyAlaCysGlnValThrSerPheSerAlaMetAlaAsn 225
QY 731 CAAGGGGAAGTCTCTTTT----- 748
Db 226 GluAlaProIleAlaPheValAlaAlaAsnValAlaGlyValArgGlyGlyIleAlaAla 245
QY 749 -----TCTCACAATCTCTTCCGATTCT----- 772
Db 246 ValGlnAspGlyGlnGlnGlyValSerSerThrSerThrGluAspProValValSer 265
QY 773 -----GGAGCTCAAT 784
Db 266 PheSerArgAsnThrAlaValGluPheAspGlyAsnValAlaArgValGlyGlyIle 285
QY 785 TTTACAGAGCGCTCGGTGACTATTCTTAATAGCTAAAGTTTCTTTATGACAAAT--- 841
Db 286 TyrSerTyrGlyAsnValAlaPheLeuAsnAsnGlyLysThrLeuPheLeuAsnVal 305
QY 842 -----AAGTCAAGGAGCGAGCTCTCCCAACAG 871
Db 306 AlaSerProValTyrIleAlaLysGlnProThrSerGlyGlnAlaSerAsnThrSer 325
QY 872 GGGGATATG---TCAGGAGGTCTATCTGTGTTATAA-----ACTAGT 913
Db 326 AsnAsnTyrGlyAspGlyGlyAlaIlePheCysLysAsnGlyAlaGlnAlaGlySerAsn 345
QY 914 ACAGATACTAAGGTCAACCTCTGGAATAGATGTTACTCTTCAAGCAATATACATCG 973
Db 346 AsnSerGlySerValSerPheAspGlyGluGlyValValPhePheSerSerAsnValAla 365
QY 974 ACAACAGCGGAGGAGTCTATCTATGAAAAGTCAAGTCTCGTTCGGAGACTTACC 1033
Db 366 AlaGlyLysGlyGlyAlaIleTyrAlaLysLysLeuSerValAlaAsnCysGlyProVal 385
QY 1034 CTATTGAGTAGAAATAGTCTCAATGAGGTACAGCTCTCTAAAGGTGGAGCCATAGTATC 1093
Db 386 GlnPheLeuArgAsnIleAlaAsn-----AspGlyGlyAlaIleTyrLeu 400
QY 1094 GAAGATAGTGGGAATGATTGTTATCCGCGATAGTGGTACATCTCTTTTAGGAAT 1153
Db 401 GlyLysGlyGlyLeuSerLeuSerAlaAspTyrGlyAspIlePheAspGlyAsn 420
QY 1154 -----ACAGTCACTTCTACTCTCTGGGACGAAT-----AGAGT 1189
Db 421 LeuLysArgThrAlaLysGluAsnAlaAlaAspValAsnGlyValThrValSerSerGln 440
QY 1190 AGTATCGACTTAGGAACGAGTGCAAGATGACAGCTTTGCGTCTCTGCTGTAGAGCC 1249
Db 441 AlaIleSerMetGlySerGlyGlyLysIleThrThrLeuArgAlaLysAlaGlyHisGln 460
QY 1250 ATCTACTTATGATCCCACTACAGGATCATCCACAACA-----GTTACA 1297
Db 461 IleLeuPheAsnAspProIleGluMetAlaAsnGlyAsnGlnProAlaGlnSerSer 480
QY 1298 GATGCTCTAAAGTAAATGAGCTCCGGCAGATTCTGCACATACTATACAGGGAACATC 1357
Db 481 LysLeuLeuLysIleAsnAspGlyGlyGly-----TyrThrGlyAspIle 495
QY 1358 ATCTTCAAGGAGAAAGTTTATCAGAGACAGGCGCCAGATTCTTAAATCTTACTTCG 1417
Db 496 ValPheAla-----AsnGlySerSer 502
QY 1418 AAGCTACTAGCCTGTAATCTTTTCAGGAGGTACTCTATCTTTAAACATGAGGTGACT 1477
Db 503 ThrLeuTyrGlnAsnValThrIleGluGlnGlnArgIleValLeuArgGluLysAlaLys 522
QY 1478 CTCGAGACTCAGGATTCATCAACAGCGAGATTCTCGTCTCGAAATGAGAGTGAAGT 1537
Db 523 LeuSerValAsnSerLeuSerGlnThrGlyGlySer---LeuTyrMetGluAlaGlySer 541

QY 1538 ACTCTAGAA-----CCTGCTGATCTAGC----- 1561
Db 542 ThrLeuAspPheValThrProGlnProGlnGlnProProAlaAlaAsnGlnLeuIle 561
QY 1562 ACCATAACAAATTTGGTCATTAAACATCAGTTCTATA----- 1597
Db 562 ThrLeuSerAsnLeuHisLeuSerLeuSerLeuLeuAlaAsnAsnAlaValThrAsn 581
QY 1598 -----GACGGTGCMAAGAGGCAAAATAGAAAACCAAGCTACG 1636
Db 582 ProProThrAsnProProAlaGlnAspSerHisProAlaValIleGlySer---ThrThr 600
QY 1637 TCAAAAATCTGACTTTATCTGGAACCATCTTATTTGGACCGCGGACGCTTTTAT 1696
Db 601 AlaGlyValThrIleSerGlyProIlePhePheGluAspLeuAspAspThrAlaTyr 620
QY 1697 GAAAATCATAGT---TTAAGAAATCCTCAGCTACGACATCTTAGAGCTCAAAGCTTCT 1753
Db 621 AspArgTyrAspTrpLeuGlySerAsnGlnLysIleAsnValLeuLysLeuGlnLeu--- 639
QY 1754 GGAATCTGAACAAGCAGCGAGTCCAGATCTTATTAATGGGTGAGAATTC---CAT 1810
Db 640 GlyThrLysProProAlaAsnAlaProSerAspLeuThrLeuGlyAsnGluMetProLys 659
QY 1811 TACGGCTATCAGGNACTTGGGCGCCAAATTGTTGGGGACAGGGCTTCTACGACTGCA 1870
Db 660 TyrGlyTyrGlnGlySerTrp---LysLeuAlaTrpAspProAsnThrAlaAsnGly 678
QY 1871 ACCTTC-----AACTGGACTAAACTGGCTATATCTTAATCCGAGCGTATC 1918
Db 679 ProTyrThrLeuLysAlaThrThrThrLysThrGlyTyrAsnProGlyProGluArgVal 698
QY 1919 GGCTTTTGTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATTAGTCTCTCATAT 1978
Db 699 AlaSerLeuValProAsnSerLeuTrpGlySerIleLeuAspIleArgSerAlaHisSer 718
QY 1979 CTTATGGAGACTGCAACGAAGGGTTCAGGAGACCGTCTTTTGGTGTGCTGGATTA 2038
Db 719 AlaIleGlnAlaSerValAspGlyArgSerTyrCysArgGlyLeuTrpValSerGlyVal 738
QY 2039 TCTAATCTTCTTCAATAGATAGTAGTACAAAACACACGCGGGTTTCGCCATTGAGTGGC 2098
Db 739 SerAsnPhePheTyrHisAspArgAspAlaLeuGlyGlnGlyTyrArgTyrIleSerGly 758
QY 2099 GGTATGTCATAGGAGGAACCTACATCTGTTTCCAGATAAGATCTTAGTCTGCTCATTT 2158
Db 759 GlyTyrSerLeuGlyAlaAsnSerTyrPheGlySer---SerMetPheGlyLeuAlaPhe 777
QY 2159 TGTACAGCTTTTGGAGAGATAGACACTACTTTGTAGCTAAGAATCAAGGTACAGCTTAC 2218
Db 778 ThrGluValPheGlyArgSerLysAspTyrValValCysArgSerAsnHisIleAlaCys 797
QY 2219 GGAGGAATCTCTATTATCCAGCACAAACGAACCTATATCTCTCTTCTTGCAAACTACGG 2278
Db 798 IleGlySerValTyrLeuSerThrGlnAlaLeu----- 809
QY 2279 CTTGTCTGTTCTTATGTTCTTCTCAGAGATCTCTGTTCTCTTTTCAGGA----- 2329
Db 810 ---CysGly---SerTyr-----LeuPheGlyAspAlaPheIle 820
QY 2330 AACCTTGTCTACCCCATACGATACGATCTGAAAACCAAGTATACACATATCTCTACT 2389
Db 821 ArgAlaSerTyrGlyPheGlyAsnGlnHisMetLysThrSerTyrThrPheAlaGluGlu 840
QY 2390 GTTAAAGGAAGCTGGGGGAATGATGTTTCGCTTTAGAAATTCGGTGGAGAGCTCCGATT 2449
Db 841 SerAspValArgTrpAspAsnAsnCysLeuAlaGlyGluIleGlyAlaGlyLeuProIle 860
QY 2450 TGCCTTAGATGAAGTCTCTATT---GAGCAGTACATCCCTTCTCATGAATTCGAGTTT 2506
Db 861 ValIleThrProSerLysLeuTyrLeuAsnGluLeuArgProPheValGlnAlaGluPhe 880

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QY 2507 GTCTATGCACATCAGGAGAGCTTTTAAAGACAGGACAGAGCTCGTGAATTGGAGT 2566
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QY 2567 AGCGCTGCTGGAATCTGCTTACCTTACCTATCGGATCGGATTTGATAGGAATCAGACTGC 2626
Db 901 GlyHisLeuLeuAsnLeuSerValProValGlyValLysPheAspArgCysSerSerThr 920
QY 2627 CAAGATCAACAGCTACATCTCTTGGTTATCTGTTGATCTGATCTGTTGATGTAACCCC 2686
Db 921 HisProAsnLysTyrSerPheMetAlaAlaTyrIleCysAspAlaTyrArgThrIleSer 940
QY 2687 GACTGTACGACACACATCGGATTTAGCGGTGATCTTTGGAAACCTTCGGTACGAATTG 2746
Db 941 GlyThrGluThrLeuLeuSerHisGlnGluThrTrpThrThrAspAlaPheHisLeu 960
QY 2747 GCACAGCAAGCTTTAGTCTCTTCGTCGAGGAAACCACTTTTCTTAACTCAAAATTTTGA 2806
Db 961 AlaArgHisGlyValValValArgGlySerMetTyrAlaSerLeuThrSerAsnIleGlu 980
QY 2807 GCCTTTAGCCAAATTTCTTTGAATTCGTCGGGTCATCTCGCAATTAACAATGTAGACTTA 2866
Db 981 ValTyrGlyHisGlyArgTyrGluTyrArgAspAlaSerArgGlyTyrGlyLeuSerAla 1000
QY 2867 GGACCAAAATACCAATTC 2884
Db 1001 GlySerLysValArgPhe 1006

RESULT 14
US-09-556-877-176
; Sequence 176 Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Vasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 176
; LENGTH: 982
; TYPE: PRN
; ORGANISM: Chlamydia
; FEATURES:
; NAME/KEY: VARIANT
; LOCATION: (1)...(982)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-556-877-176

Alignment Scores:
Pred. No.: 9.7e-91 Length: 982
Score: 1124.50 Matches: 303
Percent Similarity: 45.92% Conservative: 159
Best Local Similarity: 30.12% Mismatches: 373
Query Match: 20.79% Indels: 171
DB: 4 Gaps: 30

US-09-428-122-1 (1-3000) x US-09-556-877-176 (1-982)
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Db 23 AspProSerGlyThrThrValPheSerAlaGlyGluLeuThrLeuLysAsnLeuAspAsn 42
QY 302 ACAGGCACAGCAATCAACAAAAGCTGTTTAAACCACTAAGGCGGATTTGACTTTTCA 361
Db 43 SerIleAlaAlaLeuProLeuSerCysPheGlyAsnLeuLeuGlySerPheThrValLeu 62
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QY 362 GGTAACGGGAACCTCTATTTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCT 421
Db 63 GlyArgGlyHisSerLeuThrPheGluAsnIleArgThrSerThr---AenGlyAlaAla 81
QY 422 GTTAAACAGCAGCGCTGTAGATAAATCTACCACCTTTATAGGGTTTCTTCGCTATCTTTT 481
Db 82 LeuSerAsnSerAlaAlaAspGlyLeuPheThrIleGluGlyPheLysGluLeuSerPhe 101
QY 482 -----ATTGCTCTCTCGGAAGTTCGATACTACCGGCAAGAGCGGCTT 526
Db 102 SerAsnCysAsnSerLeuLeuAlaValLeuProAlaAlaThrThrAsnLysGlySerGln 121
QY 527 AGCTGCTCTACGGGTAGC-----TTGAGT 550
Db 122 ThrProThrThrThrSerThrProSerAsnGlyThrIleTyrSerLysThrAspLeuLeu 141
QY 551 TTGACAAAAAATGTCAGTTTGTCTCTCAGCAAAACCTTTTCAACGGATAATGCGGTGCT 610
Db 142 LeuLeuAsnAsnGluLysPheSerPheTyrSerAsnLeuValSerGlyAspGlyGlyAla 161
QY 611 ATCACCAGCAAAACTCTTTTCATTAACAGGAGCTACAAATGTACAGCTCTGTTTCTGAAAAT 670
Db 162 IleAspAlaLysSerLeuThrValGlnGlyIleSerLysLeuCysValPheGlnGluAsn 181
QY 671 ACCTCTCTCAAGAAAGCGGAGCCATTCAGACTTCGATCCCTTACCATTACTGGAAC 730
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Db 202 GluAlaProIleAlaPheValAlaAsnValAlaGlyValArgGlyGlyIleAlaAla 221
QY 749 -----TCTGCAATCTCTTCGGATCT-----772
Db 222 ValGlnAspGlyGlnGlnGlyValSerSerThrSerThrGluAspProValValSer 241
QY 773 -----GGAGTGCATTT 784
Db 242 PheSerArgAsnThrAlaValAlaGluPheAspGlyAsnValAlaArgValGlyGlyIle 261
QY 785 TTTACAGAACCTCGGTGACTATTCTTAATAATGCTAAAGTTTCTTTTATGACAAT---841
Db 262 TyrSerTyrGlyAsnValAlaPheLeuAsnAsnGlyLysThrLeuPheLeuAsnVal 281
QY 842 -----AAGTCAAGAGCGAGCTCTCAACAACG 871
Db 282 AlaSerProValTyrIleAlaAlaLysGlnProThrSerGlyGlnAlaSerAsnThrSer 301
QY 872 GGGGATATG---TCAGGAGTGTCTCTGTCGTTATAA-----ACTAGT 913
Db 302 AsnAsnTyrGlyAspGlyGlyAlaIlePheCysLysAsnGlyAlaGlnAlaGlySerAsn 321
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QY 1034 CTATTTCAGTAAATAAGTGTCAATGGAGGTACAGCTCTCTAAAGTGGAGCCATAGCTATC 1093
Db 362 GlnPheLeuArgAsnIleAlaAsn-----AspGlyGlyAlaIleTyrLeu 376
QY 1094 GAAGATAGTGGGAATAGTATTTATCCGCGAGTAGTGTGACATTTGCTTTTAGGGAAT 1153
Db 377 GlyGluSerGlyGluLeuSerLeuSerAlaAspTyrGlyAspIleIlePheAspGlyAsn 396
QY 1154 -----ACAGTCACTCTCTACTCTCTCGGAGCAAT-----AGAAGT 1189
Db 397 LeuLysArgThrAlaLysGluAsnAlaAlaAspValAlaAsnGlyValThrValSerSerGln 416
QY 1190 AGTATCGACTTAGGAACGAGTGCAGAGTTCGCTTGTGCTGCTGTAGAGCC 1249
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Db 417 AlaIleSerMetGlySerGlyGlyLysIleThrThrLeuArgAlaLysAlaGlyHisGln 436
 Qy 1250 ATCTACTCTATGATCCATACATACAGGATCATCCCAACA---GTTACA 1297
 Db 437 IleLeuPheAsnAspProIleGluMetAlaAsnGlyAsnGlnProAlaGlnSerSer 456
 Qy 1298 GATGCTTTAAAGTAATGAGATCCCGCAGATTCGCAATATACAGGGAACATC 1357
 Db 457 LysLeuLeuLysIleAsnAspGlyGlyLysIleThrGlyAspIle 471
 Qy 1358 ATCTTCACAGGAGAAAGTTATACAGAGACAGGCGCCGAGATTCATAAATCTTACTCG 1417
 Db 472 ValPheAla---AsnGlySerSer 478
 Qy 1418 AAGCTACTACAGCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAACATGGAGTGACT 1477
 Db 479 ThrLeuTyGlnAsnValThrIleGluGlnGlyArgIleValLeuArgGluLysAlaLys 498
 Qy 1478 CTGCAGACTCAGGCACTCACTCAACAGCAGATTCCTGCTCGAAATGAGCGTAGGAAC 1537
 Db 499 LeuSerValAsnSerLeuSerGlnThrGlyGlySer---LeuTyMetGluAlaGlySer 517
 Qy 1538 ACTCTAGAA---CCTGCTGATAGTACG--- 1561
 Db 518 ThrLeuAspPheValThrProGlnProGlnGlnProAlaAlaAsnGlnLeuIle 537
 Qy 1562 ACCATAAACAATTCGTTCATTAACTACATCAGTCTCTATA--- 1597
 Db 538 ThrLeuSerAsnLeuHisLeuSerLeuSerLeuLeuAlaAsnAlaValThrAsn 557
 Qy 1598 ---GACGGTGCAAGAGAGGCAAAATAGAAACCAAGCTACG 1636
 Db 558 ProProThrAsnProAlaGlnAspSerHisProAlaValIleGlySer---ThrThr 576
 Qy 1637 TCAAAAATCTGACTTATCTGCAACCATCTTATTCGACCGCGCGGACGTTTAT 1696
 Db 577 AlaGlySerValThrIleSerGlyProIlePhePheGluAspLeuAspThrAlaTy 596
 Qy 1697 GAAATCAATG---TTAAGAAATCTCAGTCTCAGCATCTTAGAGCTCAAGCTTCT 1753
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 Db 616 GlyThrLysProAlaAsnAlaProSerAspLeuThrLeuGlyAsnGluMetProLys 635
 Qy 1811 TAGCGGTATCAGGAACTGGGCGCCCAATGTTGGGGACAGGGGCTTCTACGACTGCA 1870
 Db 636 TyrGlyTyGlnGlySerTrp---LysLeuAlaTrpAspProAsnThrAlaAsnGly 654
 Qy 1871 ACCTTC-----AACTGGACTAAACTGGCTATATTCCTTAATCCCGAGCGTATC 1918
 Db 655 ProTyThrLeuLysAlaThrTrpThrLysThrGlyTyAsnProGlyProGluArgVal 674
 Qy 1919 GGCTCTTATGCTCCTATGATGGAATGCAATTTATGATATAGTCTCTCCATTTAT 1978
 Db 675 AlaSerLeuValProAsnSerLeuTrpGlySerIleLeuAspIleArgSerAlaHisSer 694
 Qy 1979 CTTATGGAGACTCAACAGGAGGTTCAGGAGACCGTCTTTTGGTGTCTGCTGATTA 2038
 Db 695 AlaIleGlnAlaSerValAspGlyArgSerTyCysArgGlyLeuTrpValSerGlyVal 714
 Qy 2039 TCTAACTCTTCTCATAGGATAGTACAAAACACAGCGGGTTCGCCATTTGAGTGGC 2098
 Db 715 SerAsnPhePheTyHisAspArgAspAlaLeuGlyGlnGlyTyArgTyIleSerGly 734
 Qy 2099 GGTATGTCATAGAGGAAACCTACATCTTGTGTTAGATTAAGATTTCTAGTGTGATTT 2158
 Db 735 GlyTySerLeuGlyAlaAsnSerTyPheGlySer---SerMetPheGlyLeuAlaPhe 753
 Qy 2159 TGTACGCTCTTGGAGAGATAGAGACTCTTTGTAGCTAAGAAATCAAGTACAGTCTAC 2218

Db 754 ThrGluValPheGlyArgSerLysAspTyValValCysArgSerAsnHisAlaCys 773
 Qy 2219 GGAGGAACCTCTCTATATACAGCAACAGAACCTATATCTCTCTCTCTGCAACTACGG 2278
 Db 774 IleGlySerValTyLeuSerThrGlnAlaLeu--- 785
 Qy 2279 CTTGTTGCTGTTCTTATGTTCTACAGAGATCTCTGTTCTCTTTTCAGGA--- 2329
 Db 786 ---CysGly---SerTy---LeuPheGlyAspAlaPheIle 796
 Qy 2330 AACCTTAGCTACACCCATACGATACGATCTGAAACCAAGTATACCAATCTCTACT 2389
 Db 797 ArgAlaSerTyGlyPheGlyAsnGlnHisMetLysThrSerTyThrPheAlaGluGlu 816
 Qy 2390 GTTAAAGGAGCTGGGGAATGATGTTTCGCTTTAGAAATTCGGTGAAGAGCTCCGATT 2449
 Db 817 SerAspValArgTrpAspAsnAsnCysLeuAlaGlyLysLeuAlaGlyLeuProIle 836
 Qy 2450 TGCTTAGTGAAGTGTCTTATTT---GAGCAGTACATGCTTTCATGAAATTCAGTTT 2506
 Db 837 ValIleThrProSerLysLeuTyLeuAsnGluLeuArgProPheValGlnAlaGluPhe 856
 Qy 2507 GTCTATGACATCAGGAGGTTTAAAGACAGGGAACAGAGCTCGTGAATTTGGAAGT 2566
 Db 857 SerTyAlaAspHisGlySerPheThrGluGluGlyAspGlnAlaArgAlaPheLysSer 876
 Qy 2567 AGCGCTCTTGTGAATCTGCTTACCTATCGGATCGGATTTGATAAGGAATCAGACTGC 2626
 Db 877 GlyHisLeuLeuAsnLeuSerValProValGlyValLysPheAspArgCysSerThr 896
 Qy 2627 CAAGATGCAAGCTCAACTTAACTCTTGTGTTATATCTGCGATCTTGTCTGATTAACCCC 2686
 Db 897 HisProAsnLysTySerPheMetAlaAlaTyIleCysAspAlaTyArgThrIleSer 916
 Qy 2687 GACTGTACGACACACTCGCAATAGCGGTGATCTCTGCGAAACCTTCGGTACGAATTTG 2746
 Db 917 GlyThrGluThrThrLeuLeuSerHisGlnGluThrTrpThrAspAlaPheHisLeu 936
 Qy 2747 GCAAGCAAGCTTGTAGTCTCTGTCGAGGAAACCATTTTCTTAACTCAAAATTTCAA 2806
 Db 937 AlaArgHisGlyValValValArgGlySerMetTyAlaSerLeuThrSerAsnIleGlu 956
 Qy 2807 GCCTTTAGCAATTTCTTTTGAATTCGGTGGGTGATCTCGCAATTCACAAATGTAGACTTA 2866
 Db 957 ValTyGlyHisGlyArgTyGlyThrArgAspAlaSerArgGlyTyGlyLeuSerAla 976
 Qy 2867 GGAGCAAAATACCAATTC 2884
 Db 977 GlySerLysVal***Phe 982

RESULT 15

US-09-620-412C-176
 ; Sequence 176, Application US/09620412C
 ; Patent No. 6448234
 ; GENERAL INFORMATION:
 ; APPLICANT: Steven P. Fling
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
 ; FILE REFERENCE: 210121.469C7
 ; CURRENT APPLICATION NUMBER: US/09/620,412C
 ; CURRENT FILING DATE: 2000-07-20
 ; NUMBER OF SEQ ID NOS: 363
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0
 ; SEQ ID NO 176
 ; LENGTH: 982
 ; TYPE: PRN
 ; ORGANISM: Chlamydia
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)...(982)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-620-412C-176

